

FIG. 1

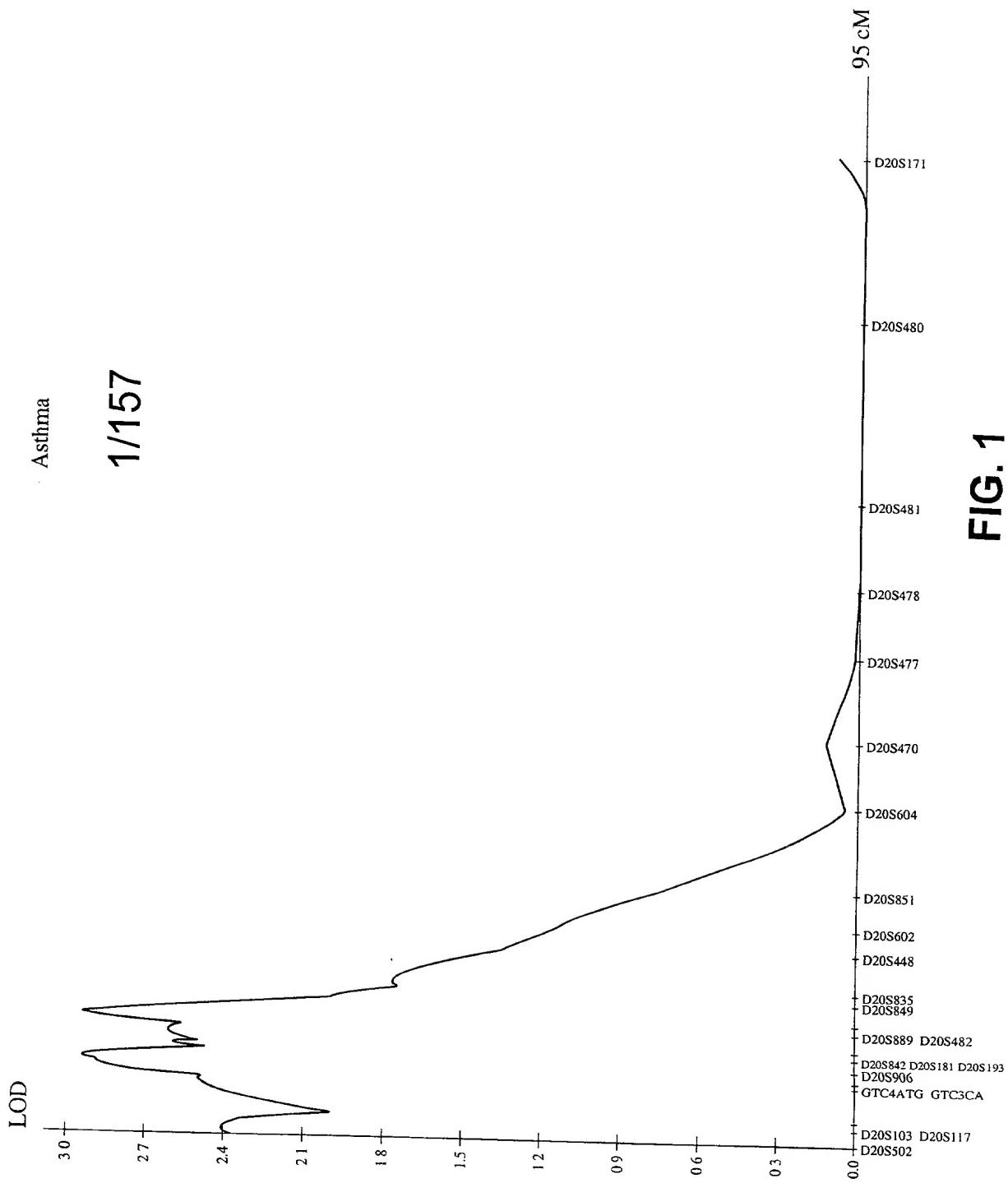


FIG. 2

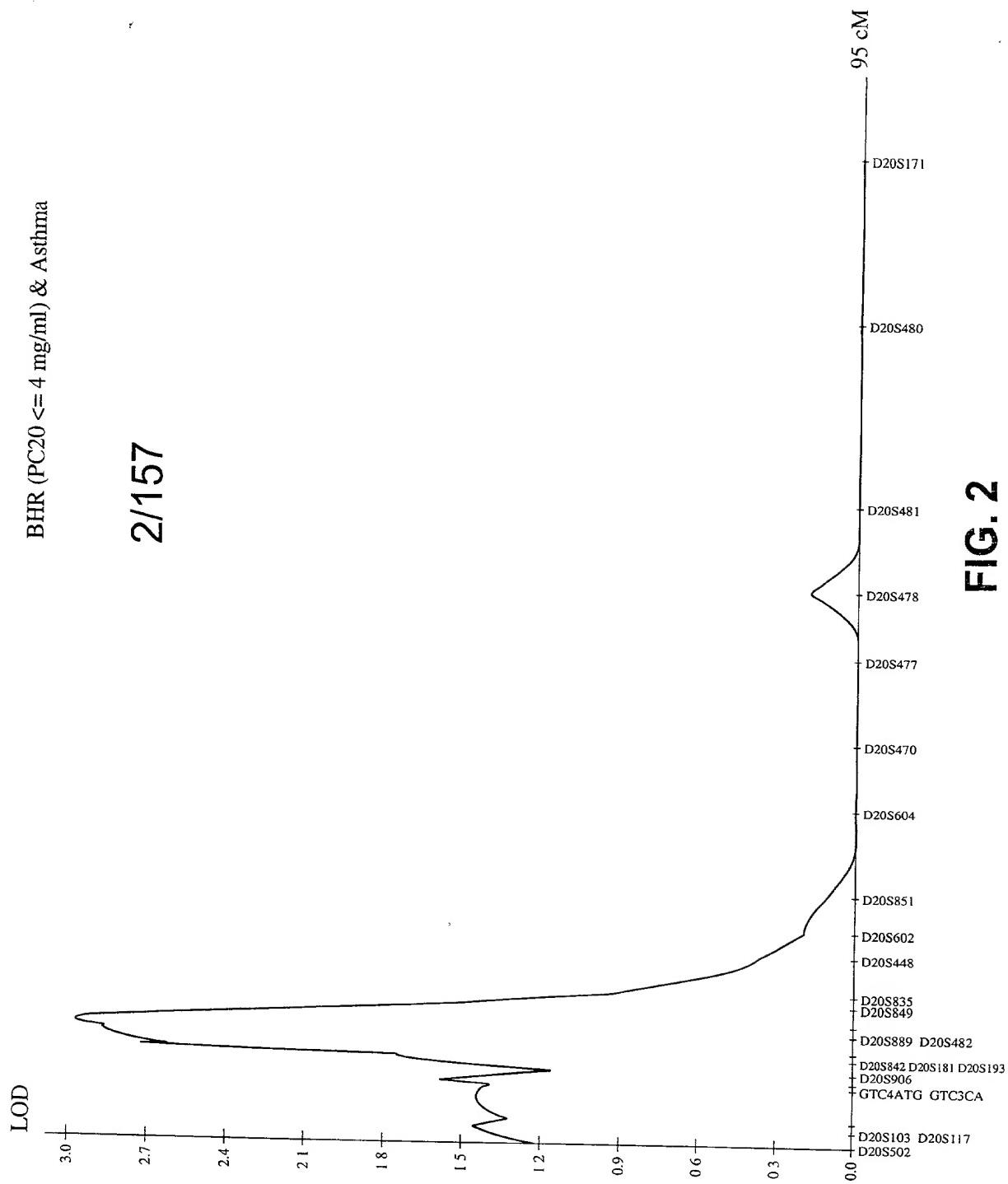


FIG. 3

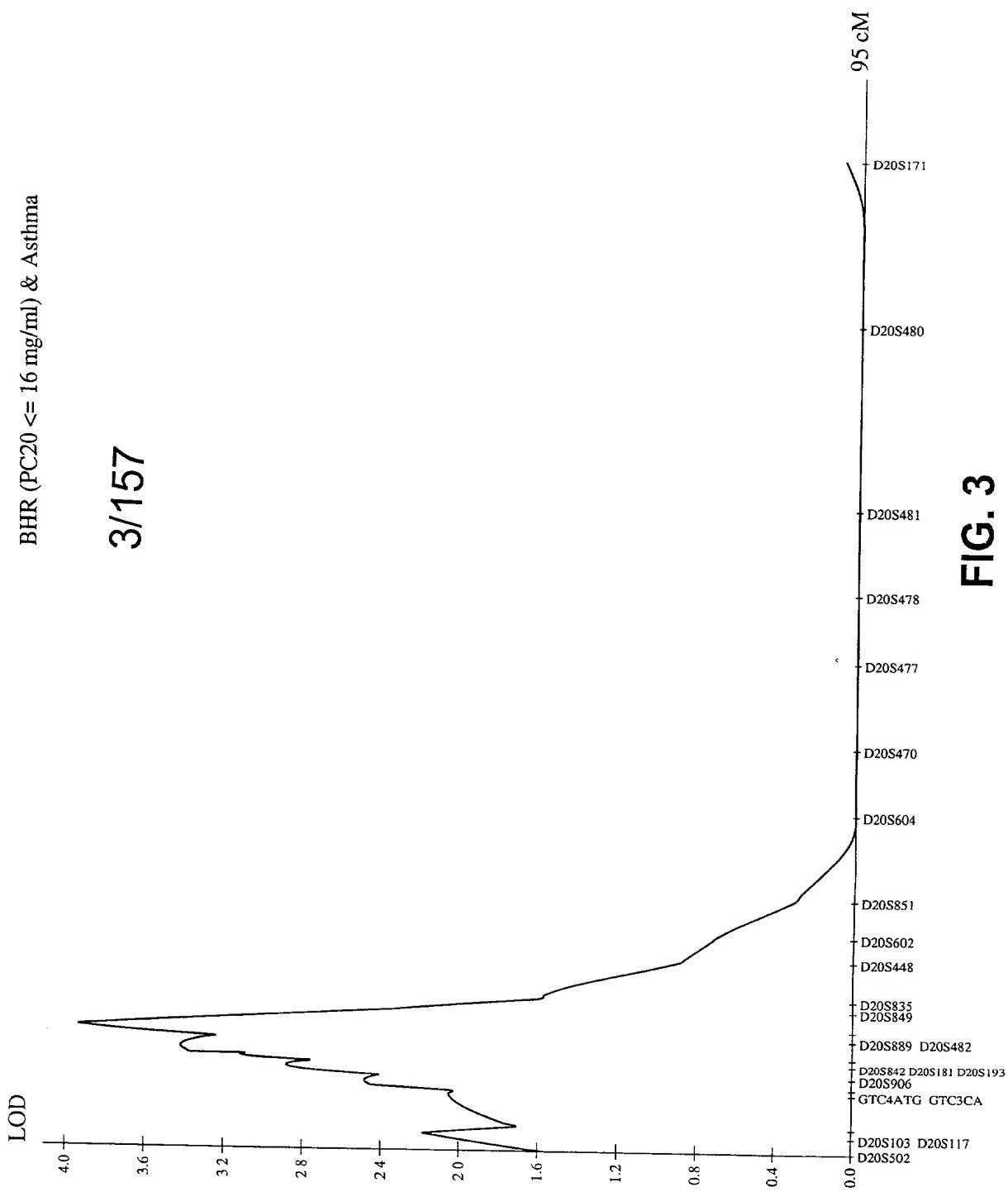


FIG. 4

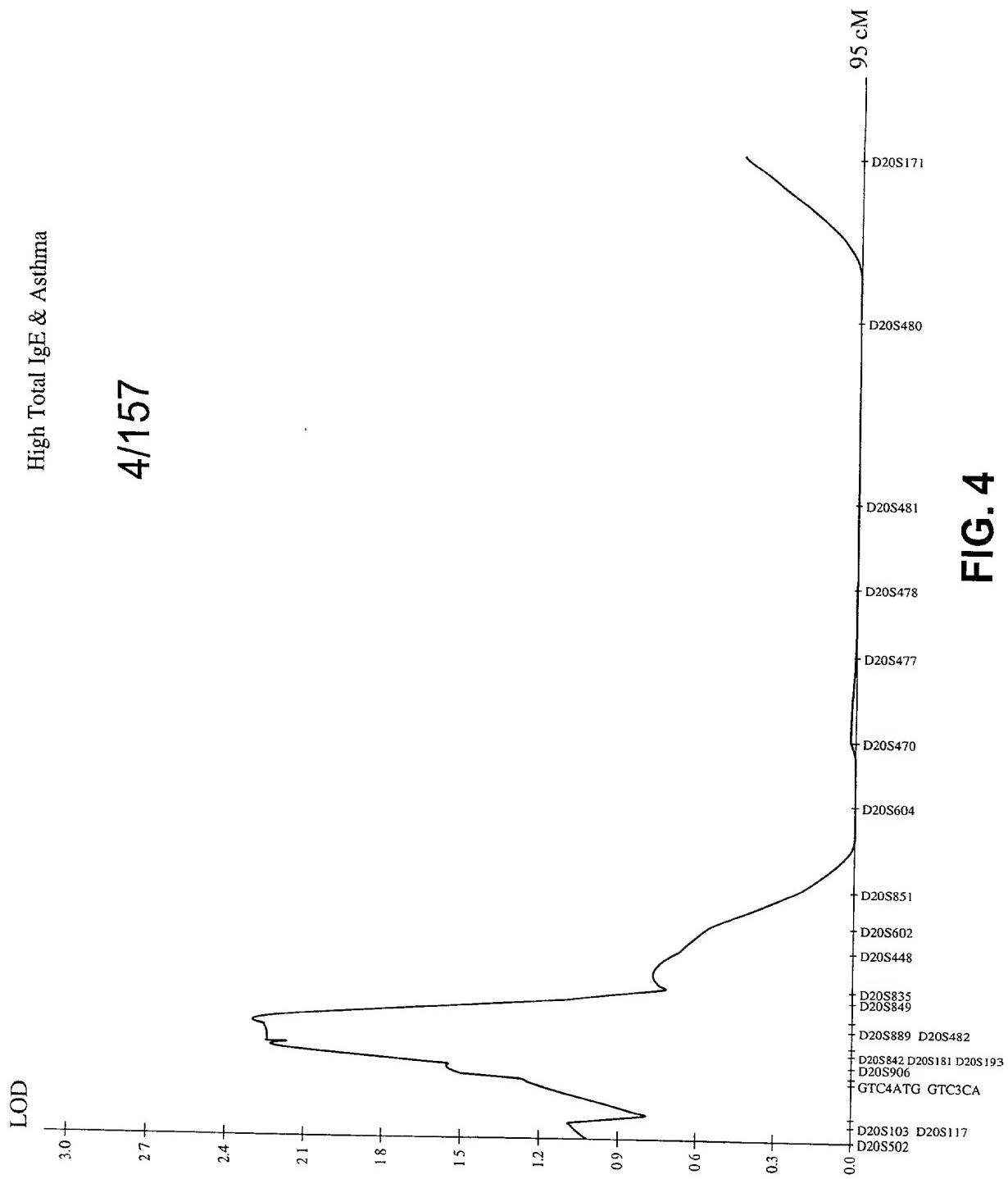
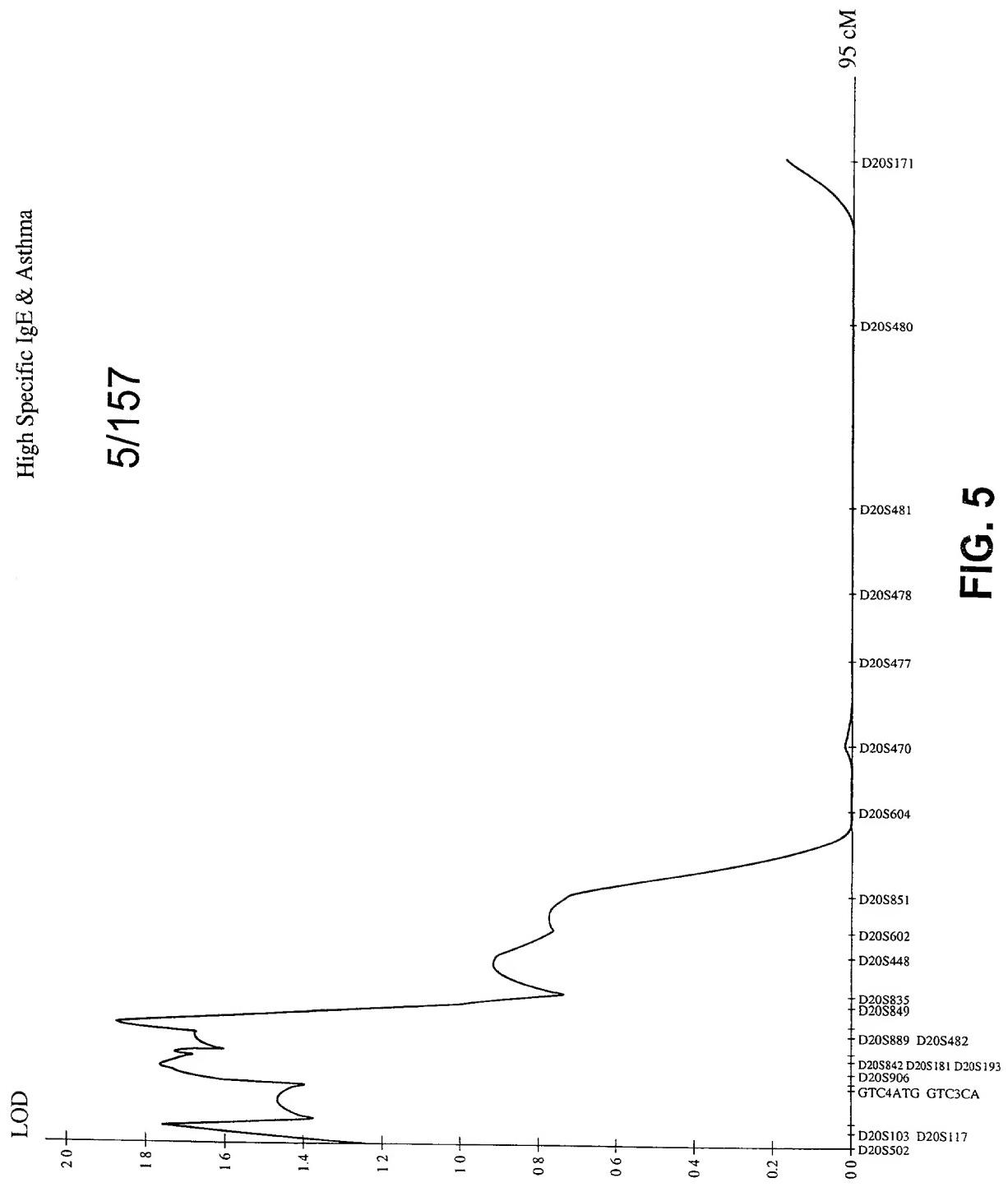


FIG. 5



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FIG. 6

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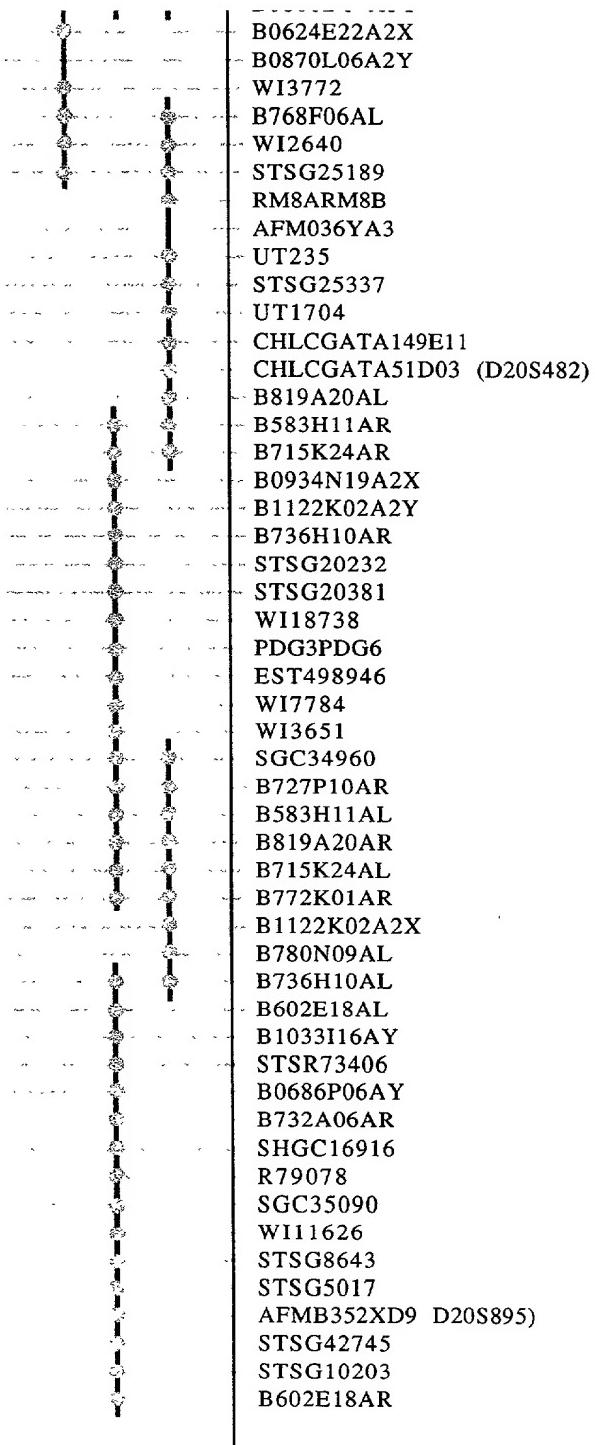


FIG. 6

FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

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FIG. 7

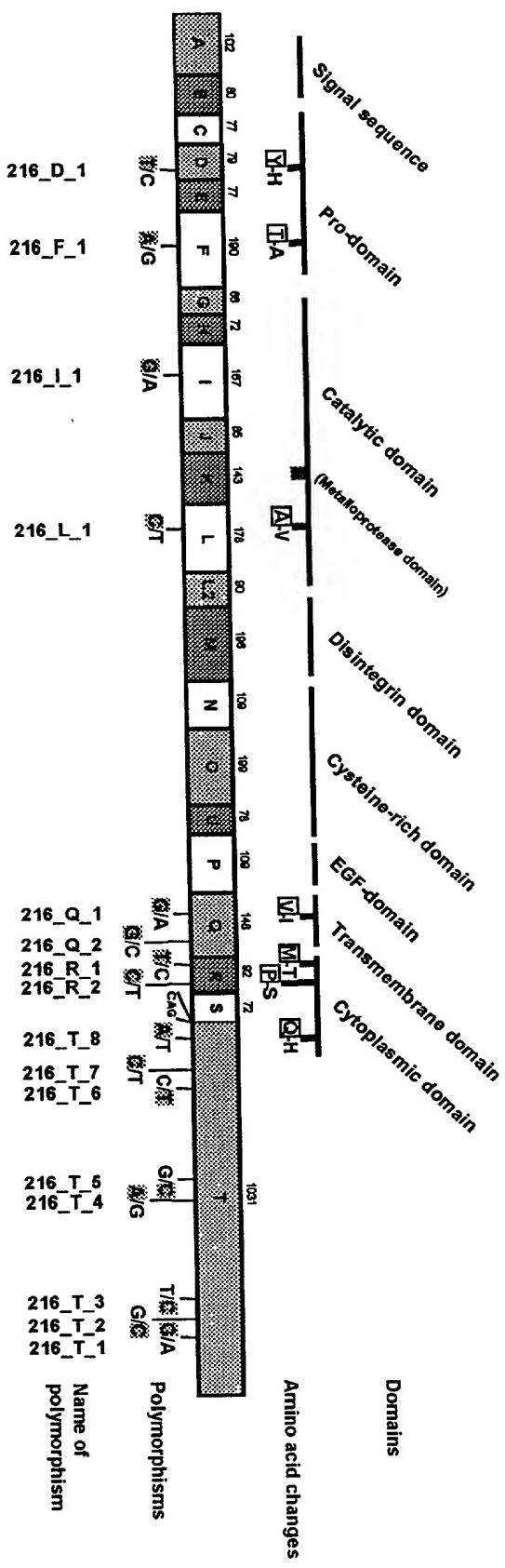


FIG. 8

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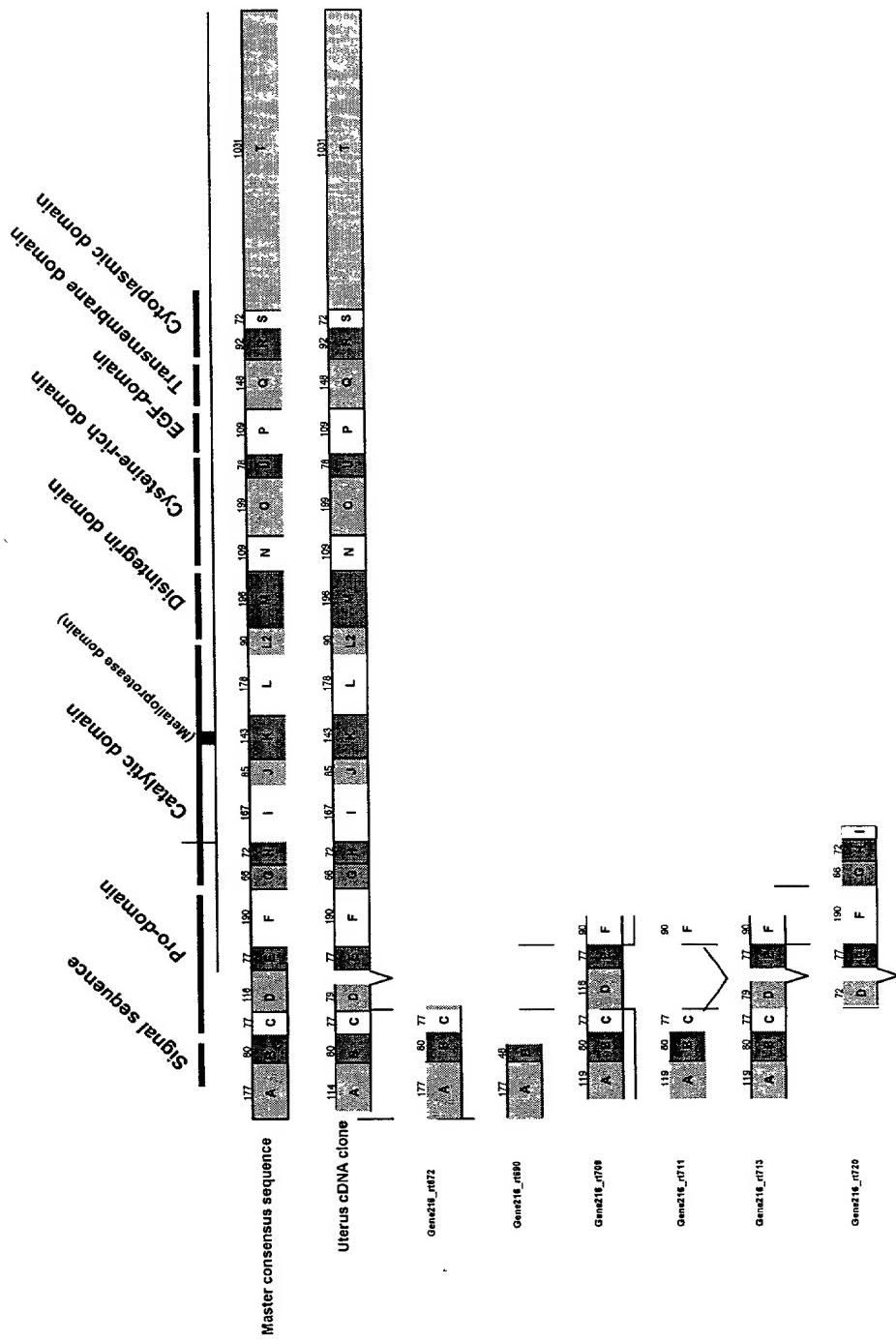


FIG. 9

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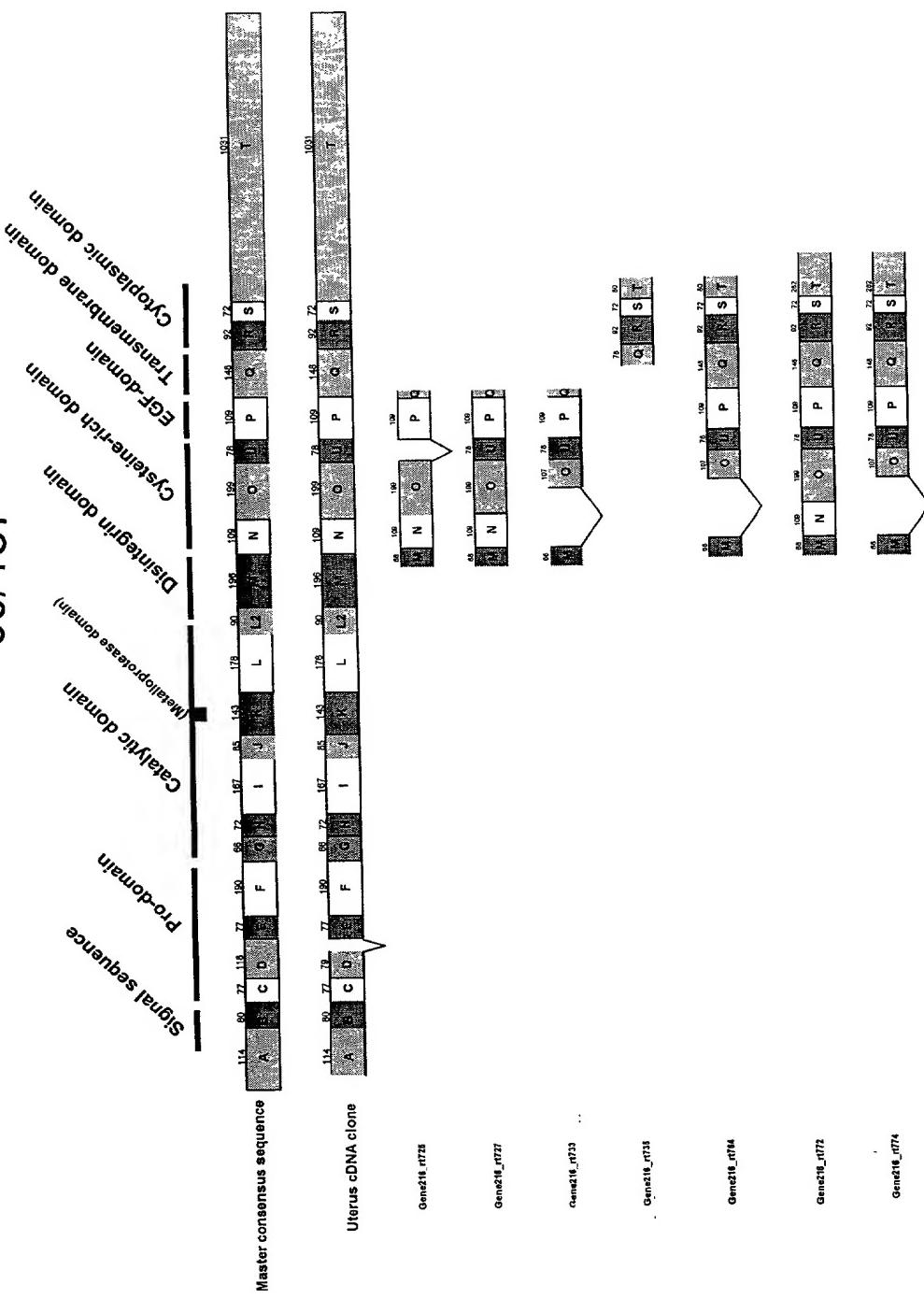


FIG. 10

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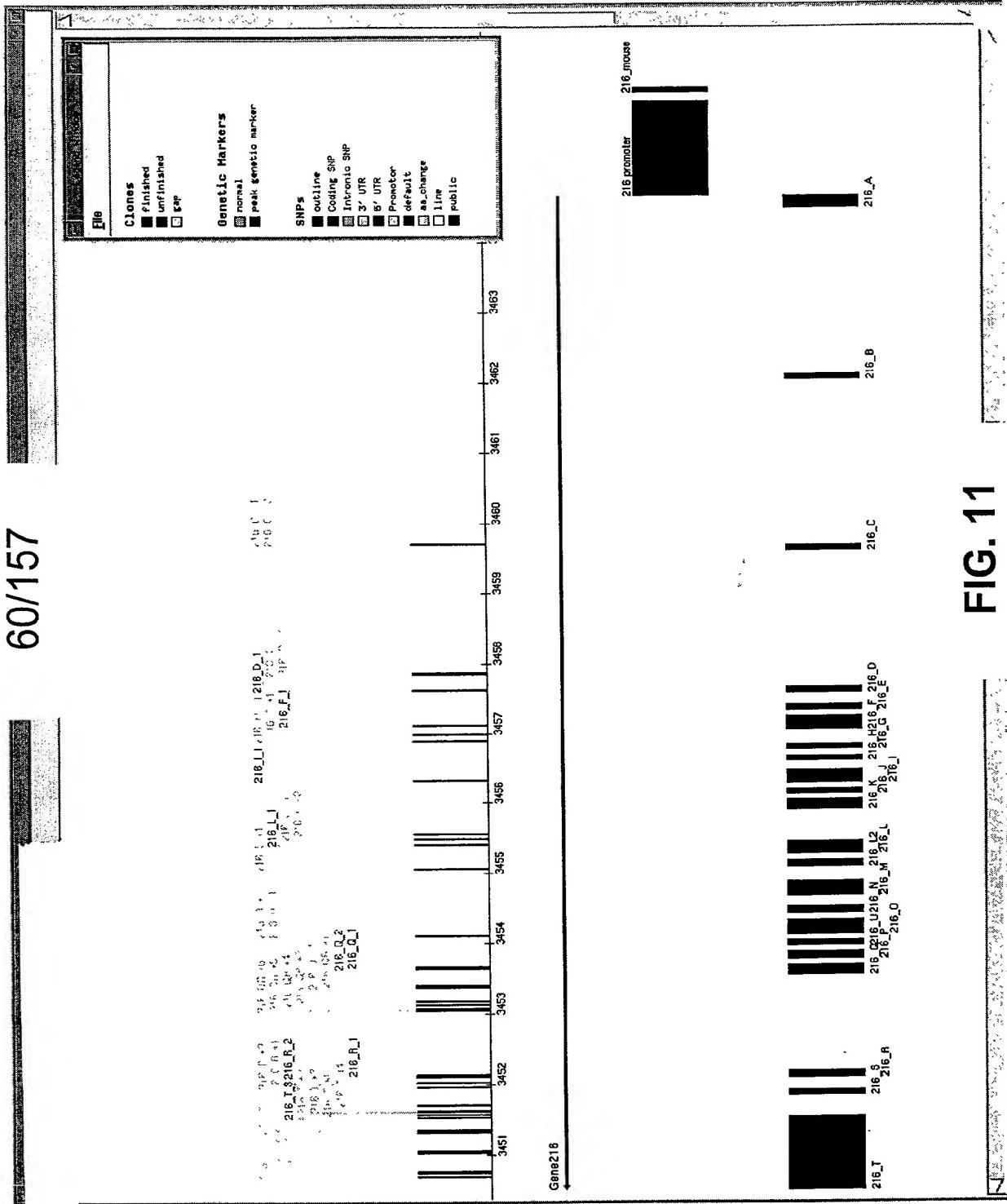


FIG. 11

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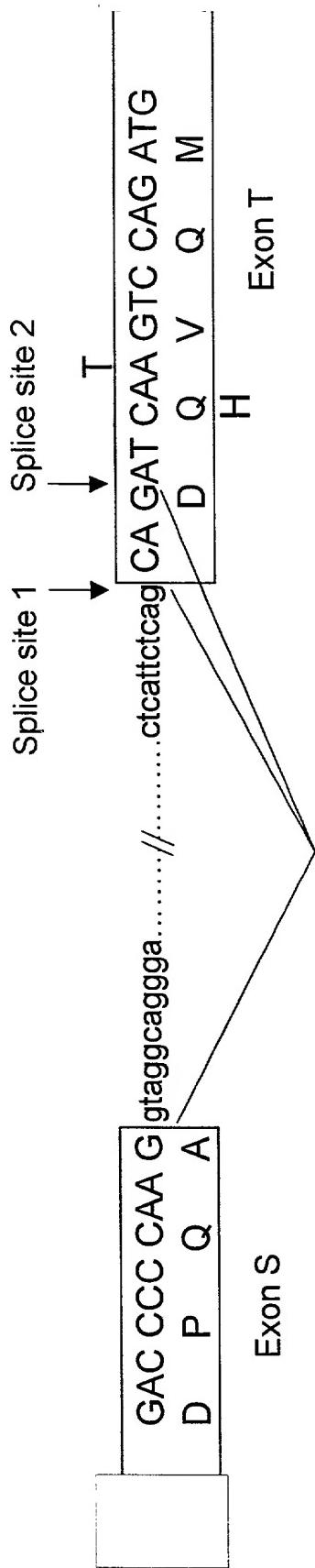


FIG. 12

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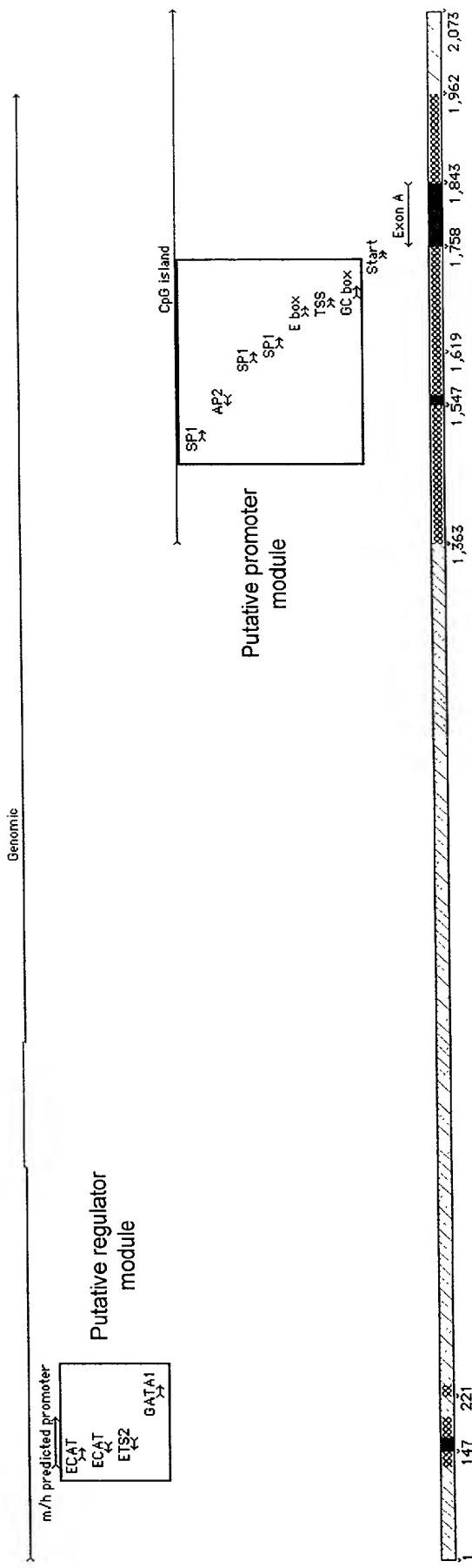


FIG. 13

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Branch of the ADAM family that Gene 216
is closely related to

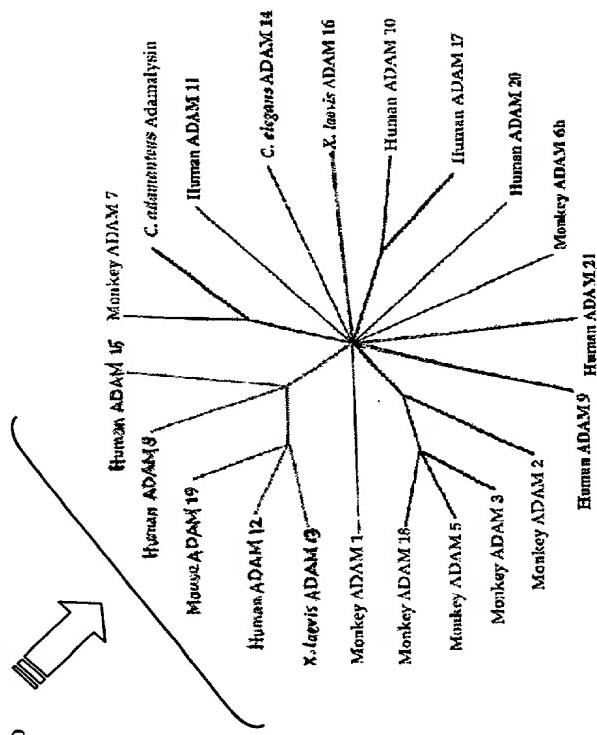


FIG. 14

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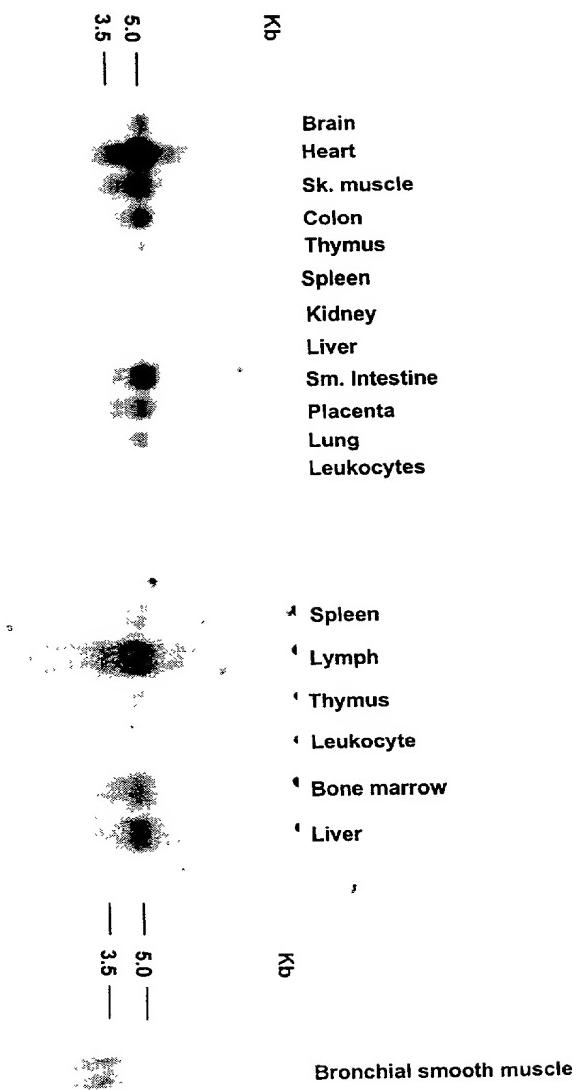


FIG. 15

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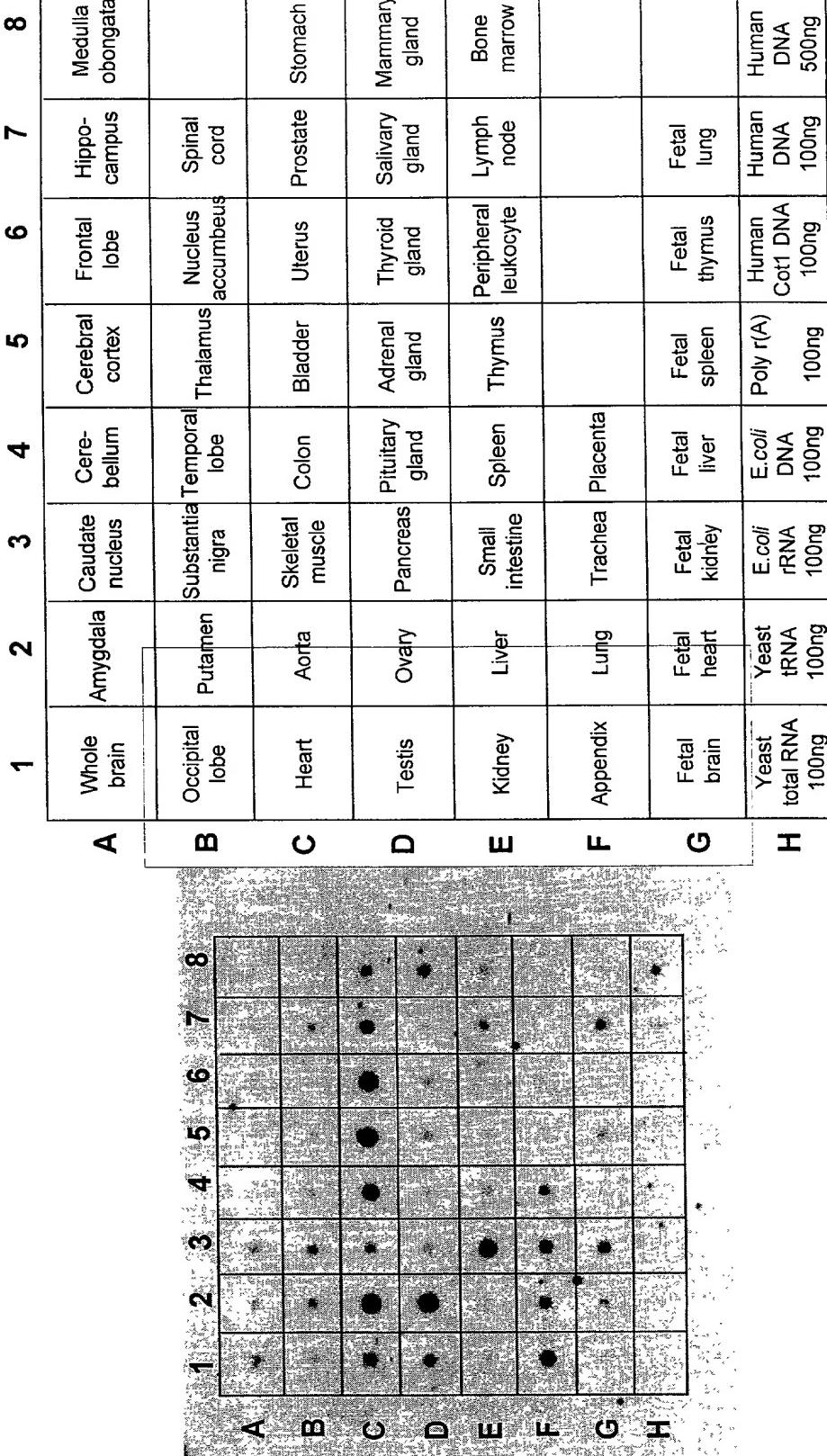


FIG. 16

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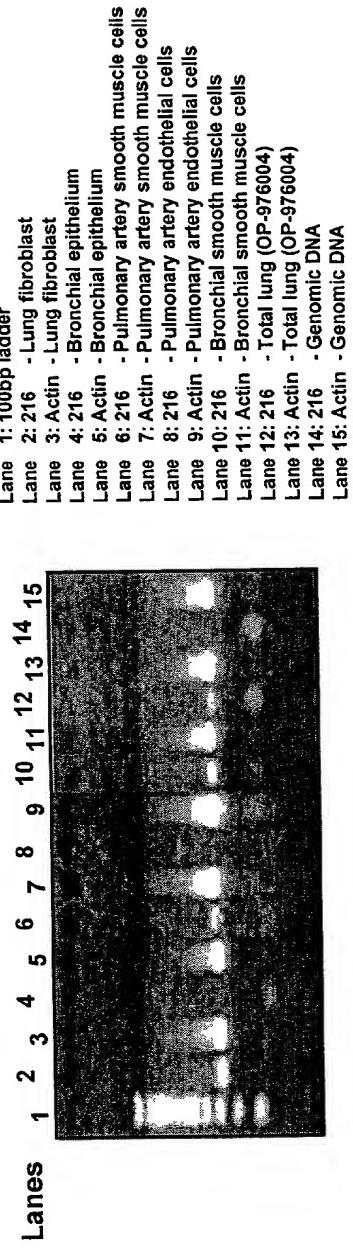


FIG. 17

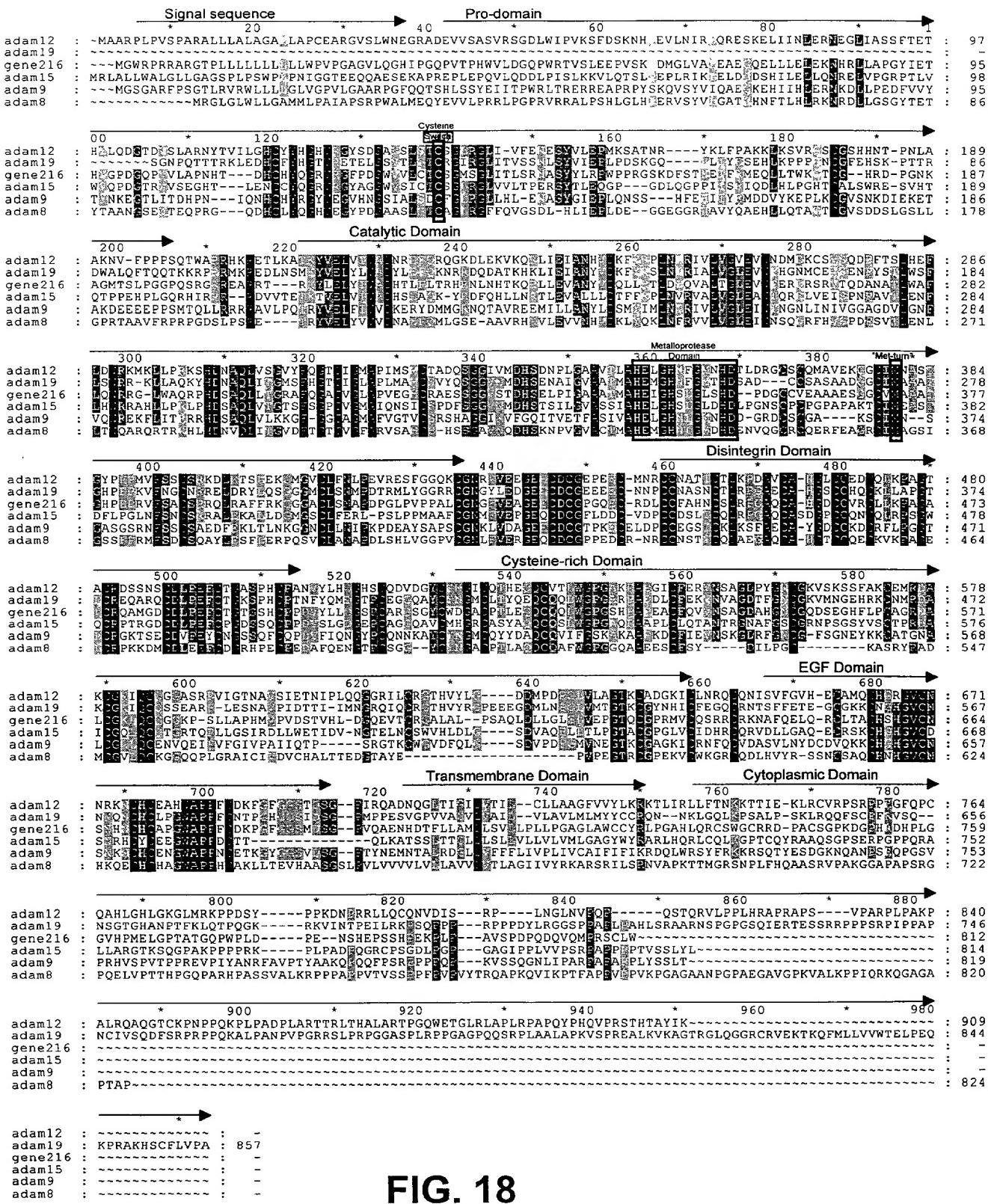


FIG. 18

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Signal sequence →
MGWRPRRARG TPLLLLLLL LLWPVPGAGV LQGHIPQPV TPHWVLGDQP 50

Pro-domain →
WRTVSLEEPV SKPDMGLVAL EAEGQELLLE LEKNHRL LAP GYIETHYGPD 100

Cysteine switch →
GQPVVLAPNH TDHCHYQGRV RGFPDSWVVL CTCSGMSGLI TLSRNASYYL 150

→ RPWPPRGSKD FSTHEIFRME QLLTWKGTCG HRDPGNKAGM TSLPGGPQSR 200
A

Catalytic Domain →
GRREARRTRK YLELYIVADH TLFLTRHRNL NHTKQRLLEV ANYVDQLLRT 250

→ LDIQVALTGL EVWTERDRSR VTQDANATLW AFLQWRRGLW AQRPHDSAQL 300

Metalloprotease →
LTGRAFQGAT VGLAPVEGMC RAESSGGVST DHSELPIGAA ATMAEIGHS 350

domain → "Met-turn"
LGLSHDPDGC CVEAAAESGG CVMAATGHP FPRVFSACSR RQLRAFFRKG 400

→ GGACLSNAPD PGLPVPPALC GNGFVEAGEE CDCGPGQECR DLCCFAHNCS 450

Disintegrin Domain →
LRPGAQCAHG DCCVRCLLKP AGALCROAMG DCDLPEFCTG TSSHCPPDVY 500

Cysteine-rich Domain →
LLDGSPCARG SGYCWDGACP TLEQQCQQQLW GPGSHPAPEA CFQVVNSAGD 550

→ AHGNCQDSE GHFLPCAGRD ALCGKLQCQG GKPSLLAPHM VPVDSTVHLD 600

→ GQEVTCRGAL ALPSAQLDLL GLGLVEPGTQ CGPRMVCQSR RCRKNAFQEL 650

EGF-like Domain →
QRCLTACHSH GVCNSHNCH CAPGWAPPFC DKPGFGGSMD SGPVQAENHD 700

Transmembrane Domain →
TFLLAMLLSV LLPLLPGAGL AWCCYRLPGA HLQRCSWGCR RDPACSGPKD 750

Cytoplasmic →
GPHRDHPLGG VHPMELGPTA TGQPWPLDPE NSHEPSSHPE KPLPAVSPDP 800

Putative SH2 binding domain T Putative casein kinase II phosphorylation site S Putative SH3 binding domain

→ QDQVQMPRSC LW **AH** 812

FIG. 19

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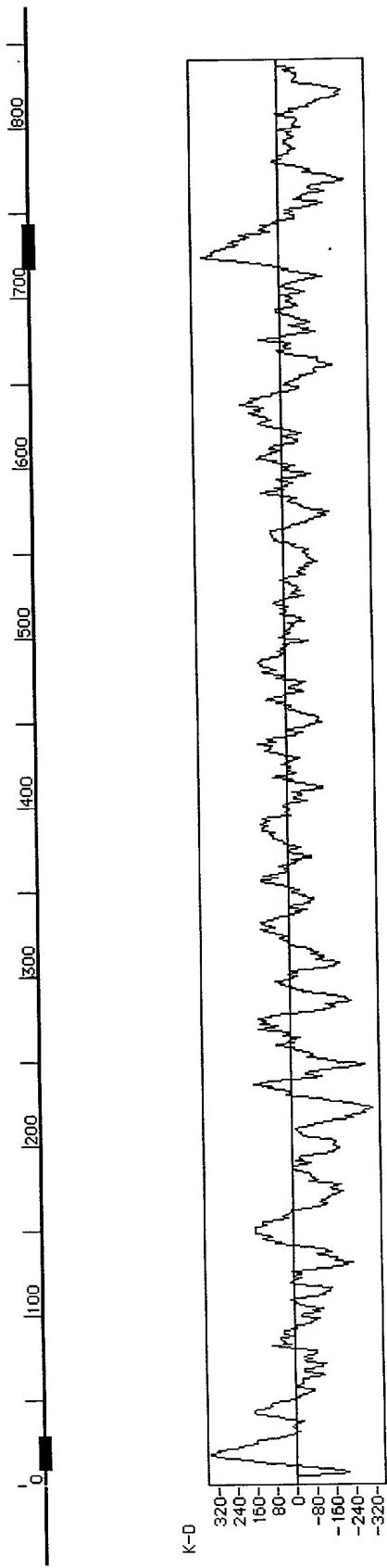


FIG. 20

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FIG. 21

FIG. 21

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FIG. 21

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FIG. 21

FIG. 21

FIG. 21

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aattttatttatcattgtatattttactgttagttataacaatgtgcataatataat
gtgtatataaaaatataatttatattatattatataatataatattatataatattaa
ttataccatatatttagtacatatacataggttacagaatgttgcacaaaagtgcagga
gccatcaaggagaagctaaaggcagcaagtgttatccctgagacgggtctgcattggac
tgtacaatttagtgttgcaggatgttgcattgttaggcaggacggagatgttgcatttt
agattcctgttgcattatgttgcattttctgttgcattttatataacatactagg
tattagcccaccgtttgaacagaatgttgcagaacaatgaagatgtactctttgtt
atgtatgttatataagacaaaatagatttttttttttttttttttttttttttttttt
tggtggcacatgccttaatccagcacttggaggcaggcaggcaggcaggatgttgc
caaggccagcgttgcactacagagtgttgcaggacagccaggctactcagagaaaactc
tgtctggaaaaaaaaaaaagagggaaaagaaaaagatttttttttttttttttttt
atgagtacaccatcagacacacaagaagaggcaccagacccattacagatgttgc
gccaccatgttgcatt
aaccctgagccatctccagccaaatagatgttgcatttttttttttttttttttttt
ataagaattcttaacttacattagtaattttaatgttgcatttttttttttttttttt
aagtcttcttaatatgaaaacttcaataagaactctgccttgcatttttttttttt
tagttgcatt
aaaaccatttaaccatgttgcatttttttttttttttttttttttttttttttttt
gaagataaaaatttgcatttttttttttttttttttttttttttttttttttttt
gacttttccataaaaactctttatgttgcatttttttttttttttttttttttttt
ccagataattactcctaatagatgttgcatttttttttttttttttttttttttt
tttgcatt
tatt
gagaaaagcttgggagcaagagcatagagcaaggcatttttttttttttttttttt
gagaaaagcttgggagcaagagcatagagcaaggcatttttttttttttttttttt

agagagcaagattagaaggagatgcagagtggaaaactataaggcaacata
 aaaaattaagagagccatatgcagaatgcagagggaaagaaaaaaaaga
 agctgcagggagagcagaaggcaggcagcttcctgaccatgggtagaacaggc
 ttttcttaataccaggcaggcttagtcttaaggataataagctttcttacaga
 cttggtttaattcattagcaataaaagtgtaaaagtgtttcttcattgcataaa
 agattggagcttatttcagccagaatgagttagtctctgcacacgggtcttgc
 tttgcattcatatacacacataagtggtgtgcgcgcattgcgtgtgtgtgt
 gt
 aaatgggacttgtgagggtatatgcataatgtgtgtgtgtgtgtgtgtgt
 atatttgcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
 agaggttattgttcaactccccctagcctgacactcgagaggcatctggacaag
 agaaaaaggcttagccattaatcctttcttagatccattttcttagagaacttcttag
 gaaactgtttagagagaacatagaaaacaggctgaaatcactgtcaaactgtcccctt
 cttcctaaggacttctactagcagactggagtttagagctgcacagtcctgaggagata
 gaacaaaggctgtttactgaatccccctgtgtttaaagatgaggcttaaaggagatt
 cagttctgaccccaaaaggaactcaggcaggctacagttatcaagatcaag
 cttaagatagggatatgtttattattaaacagctaccctaaatatctcataagatcaag
 cttaccccggtgacactccccctctgttgcctcaagaggaaccaāgagaaaccgc
 caggcgtggctcggcacaatgggttaaagatgtgttagcatgggaaatgaagagat
 ggctcagctattaagagaatatcttactcttcagaggaccagtgttcaattccagcaa
 acatatcaggtgccacaccatcactgttagctccagctgcagatctgctacatctggc
 ccataaggcacccacacacaggcgcacccacaattaaaaataagataaatctaaaaca
 gcaaaagttaaagcatgagactgtaaagtgtgtggcatagaccaagac
 ggttggccctacctgttagaaatagtctcagtatcacacaaaaggacacccaaagc
 gcaaaagctccagcaagacaaaactacagtcattcattgagagtgtgcacgctgaagacc
 gagcacactgggtgcaaaatgtacttggattctgtttgtttgtccagacagg
 ttctctgcataaacgccttggctgtccctgaaattcactgttagaccaggctggc
 aaccctcagagatccgttccccacgcattctaggctcagtcaccctgtgagatgg
 cctgaaagttgttagaaaccgcgggatctattctgacagactggctggcatcttcc
 ttctctcagcatgagattcctggggcttccatttcagcatcaagcatggtagcag
 tgAACCTGGGGCTGAGGGCTCAGACTCAGACCAACTGGAAAGCAGAGAGAACTGG
 GATTGTGGAGGGCTTGTAAACCTCAGCTCCTGCCAGCAAATACCTCCAGCAAGGCC
 CACCTCTAAACCTCCCCAACAGGGTCACCAACTGGGACCTAATATTCAAATGCCAC
 AAATATGGGAGACATGACATCCAAACCGCCAGGACAGGTGTACCTCCATGCTGGTT
 CGTAGTAAGAAAACACTAAACATTAGCCTTCTTAATAAACACTGATAATAAGCCCTG
 ATTCTCGATGTTCTCTGTCTGTCCTCCTCCACCTGCTCTGTACT
 CCTCTCTGTGTACAGATAGCCTGCCATGTCATCTGCCAGCCATGTTCTGTACT
 GCCTCTCTGCTGGACTCTCTAGATGCCTCTGGCTGTTCTCATATCTACA

>mouse Gene 216_cdna
 AAAGGCACTCCCAGC~~C~~TGGGCTCGAGGTGCGGGAGACCCGGGGTCTCG
 GTGCTGCTATTGCTGCCGCTGTTGCTGCCCTCGTGTCCGCTGCGAGCGCTCG
 GATGTTCCAGGAAATGCCATGGAGAGCTAGTC~~A~~CTCCC~~A~~CTGGATCCTGG
 AGGGCAGACTCTGGCTCAAGGT~~C~~ACCC~~T~~GGAGGAGCCGATTTGAAGCCTGAC
 TCGGTGCTGGTGGTTAGAGGCTGAAGGCCAGGATCTCTGCTTGAACTGGA
 GAAGAACACAAGCTCTGGCCCCAGGATACACAGAAACCCACTACAGGCCAG
 ATGGGCATCCGGTAGTGTGTCCCCAACCACGGATATTG~~C~~CAATATCAC
 GGGCGTGTGAGGGCTTCCGG~~A~~TCCTGGTGGTCTCAGCACCTGCTCTG
 GGATGAGTGCCTTATTGTGCTCAGCAGCAAAGTCAGCTATTATGCAACCTC
 GGACTCCTGGGATACCAAAGACTTCCAACCACAGAGATCTCCGGATGGAG
 CAGTTGTTCACCTGGAGAGGGTCCAGAGAGACAAGAACTCC~~A~~ACAAAGC
 AGGAATGGCAGTCTCTCATG~~T~~CCCCAGGCGGGTGAGGCAGAGGGCG
 CGCAGGAGTCCCAGGTACCTGGA~~A~~CTGTACATAGTGGCTGACCACACCC~~T~~GAA
 CTTGAACCAACACAGAGACAGCGCCTCTGGAGGGT~~G~~CCAATTGCGTGGACCAGA
 TTCTCAGGACTCTGGATATA~~C~~AGTTGGTGTGACGGGCTGGAAGTGTGGACC
 GAGCAGGATCTCAGTCG~~C~~ATCACTCAGGACGCAAACGAAACGCTCTGGCTT
 CCTACAGTGGCGCCGCGGGTGTGGGCCAGGAGACCACAGACTCCACACAA
 CTGCTCACGGGCCGCACCTTCCAGGGTACCA~~C~~GGTGGGCC~~T~~GGCACCTGTGG
 AGGGCATATGCCGCGGGAGAGCTCGGAGGTGTGAGCACAGACCAC~~T~~CGGA
 ACTCCCCATCGGCACAGCAGCCACCATGGCCCACGAGATAGGCCACAGCCTGG
 GCCTCCACCATGATCCC~~G~~AGGGTGTGCGTGCAGGCCATGCGAGAGCAAGG
 AGGCTGCGT~~C~~ATGGAGGCAGCCACAGGGCACCC~~T~~CCCGCGCGTCTCAGCG
 CCTGCAGCCGCCAGCTGCGCACCTTCTCGCAAA~~G~~GGGGCGGTCTTGC
 CTCTCCAACACCTCGGC~~C~~GGGGCTCTGGTGTGCCAGCCGCTGCGGAAA
 CGGCTTCTTGAAGCAGGAGAAGAGTGC~~G~~ACTGCGGTTCTGCCAGAAGTGC
 CGGACCCCTGCTGCTTTGCCACATTGCTCCCTGCGT~~C~~GGGGCTCAATG
 TGCCCACGGT~~G~~ATTGCTGTGCGAAGTGC~~C~~TGTAAAGTCCGGGGCACGCC~~T~~
 GTCGCTCTGCTGCGACTGACTGCGATCTCCCAGGTTCTG~~C~~ACCGGCACCTCC
 CCGTATTGCCCGCAGATGTTAC~~T~~ACTGGATGGCTCACCC~~T~~CGCTGAGGG
 TCGCGGCTATTGCC~~T~~AGACGGCTGGTGTCCCACGCTGGAGCAGCAGTGC~~C~~AGC
 AGCTATGGGGCTGGT~~C~~CAAGC~~G~~GGCCCCAGAGCCATGTTCCAGCAGAT
 GAACTCCATGGGAATTGCAAGGAACTGTGCCAGGACCACAAGGGTAGC
 TTCTGCC~~T~~TGTGCTAGAGGGACGCTCTGTG~~T~~GGGAAACTGCTGTGCCAGGG
 AGGGGAGCCGAACCCACTAGTGC~~C~~GCACATAGT~~G~~ACTATGGACTCCACAATT~~C~~
 TCCTAGAGGGCCGAAGTGGTTGCCAGGGGCTTGTGCTCC~~C~~AGATAGT
 CACCTGGACCAGCTTGACTTGGGCTGGTAGAGGCCAGGCC~~C~~GGCTGTGGACC
 TAGAATGGTGTGCCAGGACAGGC~~A~~CTGT~~C~~AGAATGCTACCTCCAGGAGCTGG
 AACGTTGCTGACTGCTGCCATAACGGTGGGTTTGCAATAGCAATCGTA~~A~~CT
 GTC~~A~~CTGTGCTGCTGGCTGGC~~T~~CCACCC~~T~~CTGTGACAAGCCTGGCTTGGG
 GGTAGCGTGGATAGTGGCCCTG~~C~~ACAGTC~~G~~CAAACCGAGATGCC~~T~~CC~~C~~CT
 GCCATGCTCCTCAGCTTCTGCTGCC~~T~~CTGCC~~T~~GGGGCTGGC~~T~~AGCCT
 GGTGCTACTACCAGCTCC~~A~~ACATTCTGT~~C~~ATCGAAGGGACTGTGCTGCAGG
 AGGGACCCCTATGGATAGAGACATA~~CC~~CTGGGAGTGTGC~~T~~CCGGT~~G~~GA
 GTTGGCTCCATCATCACTGGAGAGGCC~~T~~CGCCCCCTCCCCATGGACCTT~~T~~G
 CCAACAGCGTTGCACCC~~T~~CCATCTTGACTTGTCTCAGACC~~T~~CGGA~~A~~CTC
 TGAGCTTACCTAAGAACTACCC~~T~~CTGAAGCAGC~~T~~GGT~~C~~TACAGATTGAGTTCC
 AGACCTGCC~~T~~ATCC~~T~~ATGGTATGGAGACCC~~T~~GGAGACCTCTGTTGCCA
 GTCACCTACCTCTGCTCAGTTGTTGCC~~T~~CTCAGATTACAGGCTTG~~C~~AT
 CAATAAAAGAAATGAGACATGGGCC~~T~~CAGAGAASCTGTTG~~C~~ATAGAGACC~~A~~T
 ATGCTGGAAACCC~~T~~AGGGCAGGGAGGGAGACACTGTGGTTCTTCTGGGTC
 CTTATAGAGGGAGGACAAATGTGCC~~T~~GCCATGTGACTTG~~C~~AGTCCTCAGTTTC
 TCAGACGC~~A~~CTCTTATAATTCTATGGGCTGTATGCTGAGGCTCTACTCAGCATA
 GGAACCC~~C~~AGAGGCCGATCATGTTGATCCSCCTGCC~~T~~GAGAGCTGTGCTAT
 TCTGAAATGTTAGAATGTATCTAATAACAATAAA~~T~~CCACAAGTTATCAGHAAA
 AAAAAAAA

FIG. 22

>mouse_Gene_216_protein
MGSRCGRPGGSPVLLLPLLLPSCLRSARMFPGNAHGELVTPHWILEGRWLKVTLLEPILKPDSDLVALEAEGQDLLL
ELEKKHKLLAPGYTETHYRPDGHPVVLSPNHTDHQCQYHGRVRGFRESWVLSTCSGMSGGLIVLSSKVSYYLQPRTPGDTK
DFPTHEIFRMEQLFTWRGVQRDKNSQYKAGMASLPHVPQSRRVREARRSPRYLELYIVADHTLNLNHTRQRLLLEVANCVD
QILRTLDIQLVLTGLEVWTEQDLSRITQDANETLWAFLQWRRGVWARRPHDSTQLTGRTFQGTTVGLAPVEGICRAESS
GGVSTDHSELPIGTAATMAHEIGHSLGLHHDPGCCVQADAEQGGCVMEAATGHPPPRVFSACSRRLRTRKGGGPCL
SNTSAPGLLVLPSRCGNGFLEAGEECDCGSGQKCPDPCCFAHNCSLRAGAQCAHGDCCAKCLLKSAGTPCRPAATDCDLP
EFCTGTSPYCPADVYLLDGSPCAEGRGYCLDGWCPTLEQQCQQLWGPGSKPAPEPCFQQMNMSMGNSQGNCGQDHKGSLP
CAQRDALCGKLLCQGGEPNPLVPHIVTMDSTILLEGREVVCRGAFVLPDSHLDQLDLGLVEPGTGCGRMVCQDRHCQNA
TSQEALERCLTACHNGGVCNSNRNCHCAAGWAPPFCDKPGLGGSVDSGPQAQSANRDAFPLAMLLSFLLPLPGAGLAWCYY
QLPTFCHRRGLCCRDPWNRDIPLGSVHPVEFGSIITGEPSPPPPWTSCQORSHPPSLLDLSDPANSELT

FIG. 22

FIG. 23

FIG. 23

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10	30	50
CGGGCACGGGTCGGCCGAATCCAGCCTGGCGGAGCCGGAGTTGCAGGCCGTGCCTAG -----+-----+-----+-----+-----+-----+		
70	90	110
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTGGGGACCCGTTGC -----+-----+-----+-----+-----+-----+ MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL		
130	150	170
TGCTGCTGCTACTACTGCTGCTCTGGCCAGTGCCAGGCGCCGGGTGCTTCAAGGAC -----+-----+-----+-----+-----+-----+ euLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH		
190	210	230
ATATCCCTGGCAGCCAGTCACCCCGCACTGGGT CCTGGATGGACAACCCTGGCGCACCG -----+-----+-----+-----+-----+-----+ isileProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThrV		
250	270	290
TCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGCTGGTGGCCCTGGAGGCTGAAG -----+-----+-----+-----+-----+-----+ alSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluG		
310	330	350
GCCAGGAGCTCCTGTTGAGCTGGAGAAGAACACAGGCTGCTGGCCCCAGGATAACATAG -----+-----+-----+-----+-----+-----+ lyGlnGluLeuLeuLeuGluLeuLysAsnHisArgLeuLeuAlaProGlyTyrIleG		
370	390	410
AAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCCCCAACACACGGTGAGAT -----+-----+-----+-----+-----+-----+ luThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrValArgC		
430	450	470
GCTTCCATGGGCTCTGGGATGCACCGCCAGAGGATCATTGCCACTACCAAGGGCGAGTAA -----+-----+-----+-----+-----+-----+ ysPheHisGlyLeuTrpAspAlaProProGluAspHisCysHisTyrGlnGlyArgValA		

FIG. 24

490 510 530

GGGGCTTCCCCACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCCTGATCA
 -----+-----+-----+-----+-----+
 rgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyLeuIleT

550 570 590

CCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCGGGGCTCCAAGGACT
 -----+-----+-----+-----+-----+
 hrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspP

610 630 650

TCTCAACCCACGAGATCTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCC
 -----+-----+-----+-----+-----+
 heSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrCysGlyH

670 690 710

ACAGGGATCCTGGAACAAAGCGGGCATGACCAGCCTCCTGGTGGTCCCAGAGCAGGG
 -----+-----+-----+-----+-----+
 isArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnSerArgG

730 750 770

GCAGGCGAGAACGCGCGAGGACCCGGAAGTACCTGAACTGTACATTGTGGCAGACCACA
 -----+-----+-----+-----+-----+
 lyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaAspHisT

790 810 830

CCCTGTTCTGACTCGGCACCGAAACTTGAACCACACCAAACAGCGTCTCCTGGAAAGTCG
 -----+-----+-----+-----+-----+
 hrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuGluValA

850 870 890

CCAACTACGTGGACCAGCTCTCAGGACTCTGGACATTAGGTGGCGCTGACCGGCCTGG
 -----+-----+-----+-----+-----+
 laAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrGlyLeuG

910 930 950

AGGTGTGGACCGAGCGGGACCCGAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGG
 -----+-----+-----+-----+-----+
 luValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrLeuTrpA

970 990 1010

FIG. 24

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CCTTCCTGCAGTGGCGCCGGGGCTGTGGCGCAGCGGCCCCACGACTCCGCAGCTGC
-----+-----+-----+-----+-----+-----+
laPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaGlnLeuL

1030 1050 1070
TCACGGGCCGCGCTTCCAGGGGCCACAGTGGGGCCTGGCGCCGTCGAGGGCATGTGCC
-----+-----+-----+-----+-----+
euThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyMetCysA

1090 1110 1130
GCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCGCCGCAG
-----+-----+-----+-----+-----+
rgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyAlaAlaA

1150 1170 1190
CCACCATGGCCCATGAGATCGGCCACAGCCTCGGCTCAGCCACGACCCCGACGGCTGCT
-----+-----+-----+-----+-----+
laThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspGlyCysC

1210 1230 1250
GCGTGGAGGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGCCACCGGGCACCCGT
-----+-----+-----+-----+-----+
ysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyHisProP

1270 1290 1310
TTCCGCGCGTGTTCAGCGCCTGCAGCCGCCCCAGCTGCGCGCTTCTTCCGCAAGGGGG
-----+-----+-----+-----+-----+
heProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgLysGlyG

1330 1350 1370
GCGGCGCTTGCCTCTCCAATGCCCCGGACCCCGGACTCCCGGTGCCGCCGGCGCTCTGCG
-----+-----+-----+-----+-----+
lyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaLeuCysG

1390 1410 1430
GGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGAGTGCCG
-----+-----+-----+-----+-----+
lyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluCysArgA

1450 1470 1490

FIG. 24

ACCTCTGCTGCTTGCTCACAACTGCTCGCTGCCGCCGGGGCCCAGTGCAGCCCACGGGG
 +-----+-----+-----+-----+-----+-----+
 spLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaHisGlyA

1510	1530	1550
------	------	------

ACTGCTGCGTGGCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTG
 +-----+-----+-----+-----+-----+-----+
 spCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaMetGlyA

1570	1590	1610
------	------	------

ACTGTGACCTCCCTGAGTTTGACGGGCACCTCCCTCCACTGTCCCCCAGACGTTTACC
 +-----+-----+-----+-----+-----+-----+
 spCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspValTyrL

1630	1650	1670
------	------	------

TACTGGACGGCTCACCTGTGCCAGGGCAGTGGCTACTGCTGGATGGCGCATGTCCA
 +-----+-----+-----+-----+-----+-----+
 euLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaCysProT

1690	1710	1730
------	------	------

CGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGCCTGGCTCCACCCAGCTCCGAGGCCT
 +-----+-----+-----+-----+-----+-----+
 hrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProGluAlaC

1750	1770	1790
------	------	------

GTTTCCAGGTGGTGAACCTCTGCCGGAGATGCTCATGGAAACTGCCAGGACAGCGAGG
 +-----+-----+-----+-----+-----+-----+
 ysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspSerGluG

1810	1830	1850
------	------	------

GCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGGAAAGCTGCAGTGCCAGGGTG
 +-----+-----+-----+-----+-----+-----+
 lyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysGlnGlyG

1870	1890	1910
------	------	------

GAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACCTAGATG
 +-----+-----+-----+-----+-----+-----+
 lyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisLeuAspG

1930	1950	1970
------	------	------

GCCAGGAAGTGACTTGTGGGGAGCCTGGCACTCCCCAGTGCCAGCTGGACCTGCTTG

FIG. 24

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-----+-----+-----+-----+-----+
lyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspLeuG

1990

2010

2030

GCCTGGGCCTGGTAGAGGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGAGCAGGC
-----+-----+-----+-----+-----+
lyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnSerArgA

2050

2070

2090

GCTGCAGGAAGAACATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACG
-----+-----+-----+-----+-----+
rgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisSerHisG

2110

2130

2150

GGGTTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGCTCCACCCTCTGTG
-----+-----+-----+-----+-----+
lyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProPheCysA

2170

2190

2210

ACAAGCCAGGCTTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACA
-----+-----+-----+-----+-----+
spLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGluAsnHisAspT

2230

2250

2270

CCTTCCTGCTGGCCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGGGGCCGGCTGG
-----+-----+-----+-----+-----+
hrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGlyAlaGlyLeuA

2290

2310

2330

CCTGGTGTGCTACCGACTCCCAGGAGCCATCTGCAGCGATGCAGCTGGGGCTGCAGAA
-----+-----+-----+-----+-----+
laTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysArgA

2350

2370

2390

GGGACCCCTGCGTGCAGTGGCCCCAAAGATGGCCCACACAGGGACCACCCCTGGCGGCG
-----+-----+-----+-----+-----+
rgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGlyV

2410

2430

2450

TTCACCCCATGGAGTTGGCCCCACAGCCACTGGACAGCCCTGGCCCCCTGGACCCTGAGA
-----+-----+-----+-----+-----+

FIG. 24

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alHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspProGluA

2470

2490

2510

ACTCTCATGAGCCCAGCAGCCACCCCTGAGAAGCCTCTGCCAGCAGTCTGCCTGACCCCC
-----+-----+-----+-----+-----+-----+
snSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProAspProG

2530

2550

2570

AAGCAGATCAGTCCAGATGCCAAGATCCTGCCCTGGTGAGAGGTAGCTCCTAAAATGA
-----+-----+-----+-----+-----+-----+
lnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

2590

2610

2630

ACAGATTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACTGAACTGCAGGGCAG
-----+-----+-----+-----+-----+-----+

2650

2670

2690

AGCCAGTGAATCACCGGACCTCCAGCACTGCAGGCAGCTTGGAAGTTCTTCCCCGAGT
-----+-----+-----+-----+-----+-----+

2710

2730

2750

GGAGCTTCGACCCACCCCACTCCAGGAACCCAGAGCCACATTGAAGTTCCTGAGGGCTGG
-----+-----+-----+-----+-----+-----+

2770

2790

2810

AGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGGTCA
-----+-----+-----+-----+-----+-----+

2830

2850

2870

CACAGCCCCTGACCTCCCTACCAGTGGAGGCTGGGTAGTGCTGGCCATCCCAAAAGGGC
-----+-----+-----+-----+-----+-----+

2890

2910

2930

TCTGTCTGGAGTCTGGTGTCTCCTACATGCATTCCACGGACCCAGCTCTGTGGA
-----+-----+-----+-----+-----+-----+

2950

2970

2990

GGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGTTCACTGAGTCCAC
-----+-----+-----+-----+-----+-----+

FIG. 24

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3010 3030 3050
ACTCCCCTGCAGCCTGGCTGGCCTCTGCAAACAAACATAATTTGGGACCTTCCTCCT
-----+-----+-----+-----+-----+-----+

3070 3090 3110
GTTTCTTCCCACCCTGTCTTCTCCCTAGGTGGTTCTGAGCCCCCACCCCCAATCCCAG
-----+-----+-----+-----+-----+-----+-----+

3130 3150 3170
TGCTACACCTGAGGTTCTGGAGCTCAGAACATCTGACAGCCTCTCCCCATTCTGTGTGT
-----+-----+-----+-----+-----+-----+-----+

3190 3210 3230
CGGGGGGACAGAGGGAACCAATTAAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACA
-----+-----+-----+-----+-----+-----+-----+

3250 3270 3290
TGTTGGCTATAGGCGTGGCTCATGCCTATAATCCAGCACTTGGGAAGCGGGTA
-----+-----+-----+-----+-----+-----+-----+

3310 3330 3350
GGAGGATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGCAACACAGCAAGACACCGCA
-----+-----+-----+-----+-----+-----+-----+

3370 3390 3410
TCTACAGAAAAATTAAAATTAGCTGGCGTGGTGTGTACCTGTAGGCCTAGCTGC
-----+-----+-----+-----+-----+-----+-----+

3430 3450 3470
TCAGGAGGCTGAAGCAGGAGGATCATTGAGCCTGAGTCAACACTGCAGTGAGCTATGG
-----+-----+-----+-----+-----+-----+-----+

3490 3510 3530
TGGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCGTCTCTAAATAAATT
-----+-----+-----+-----+-----+-----+-----+

3550 3570 3590

FIG. 24

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AAAAAAGACATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+

3610

AAAAAAAAAAAAAAAAAAAAAA
-----+-----+

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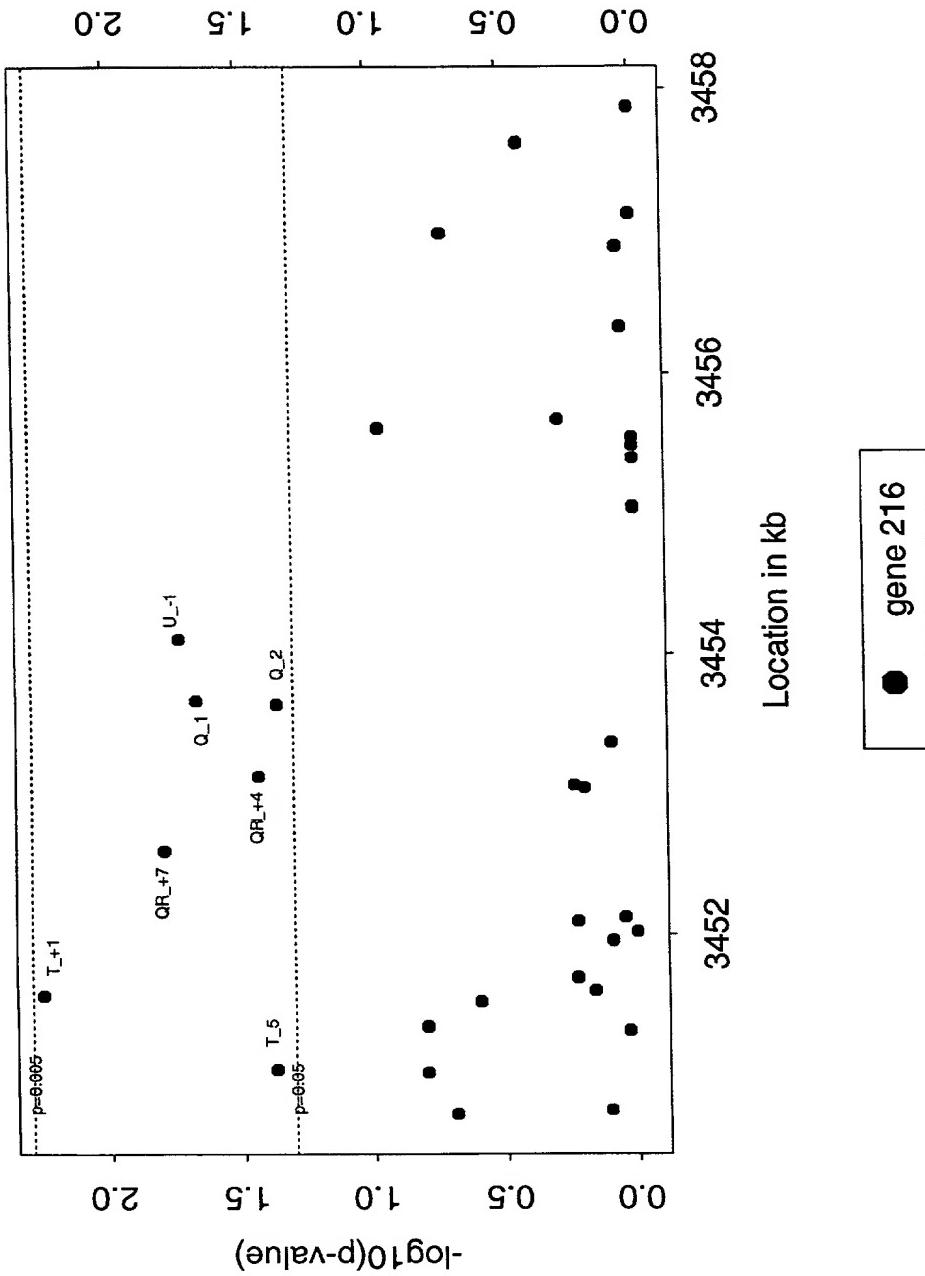
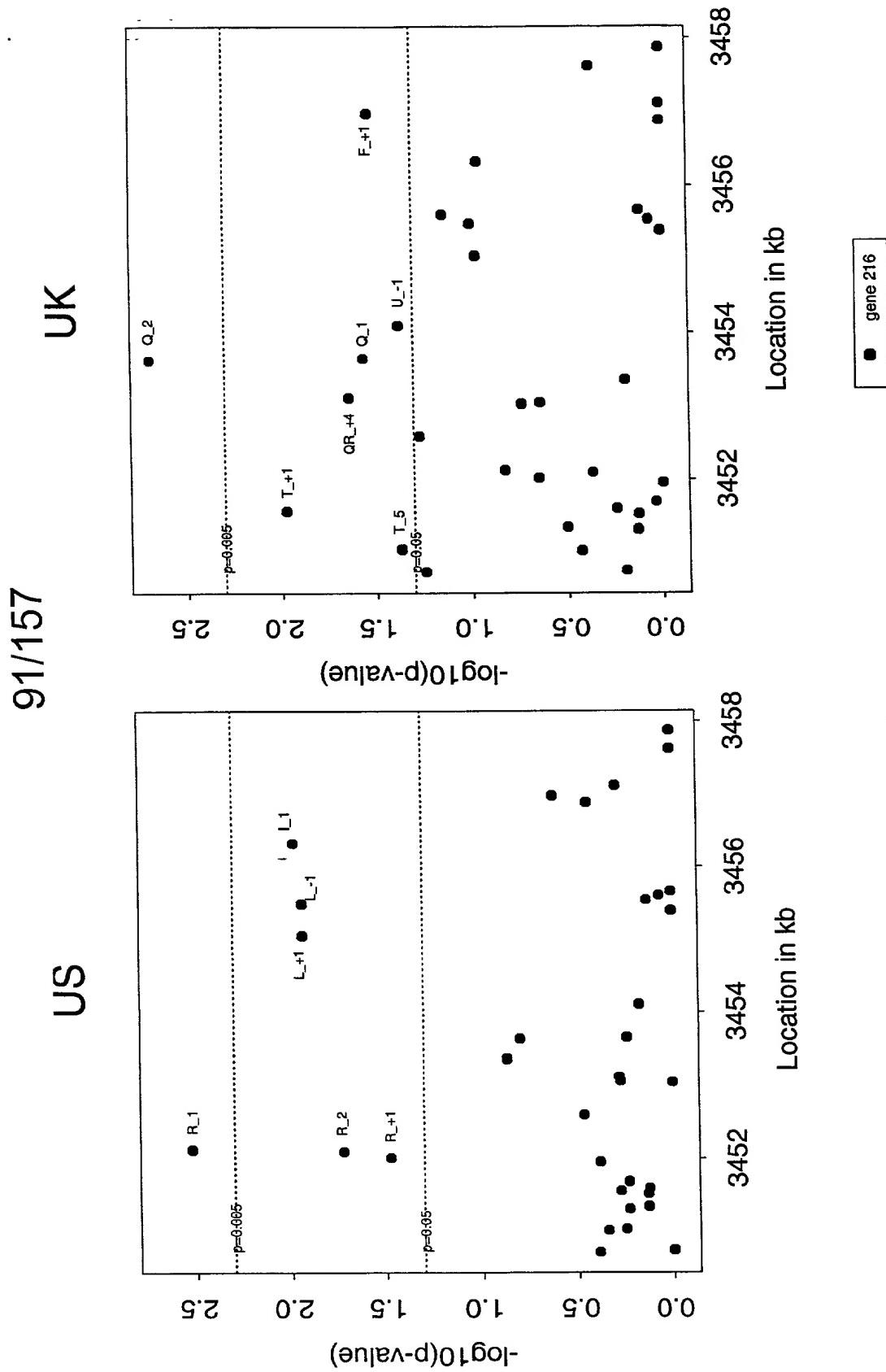


FIG. 25

FIG. 26



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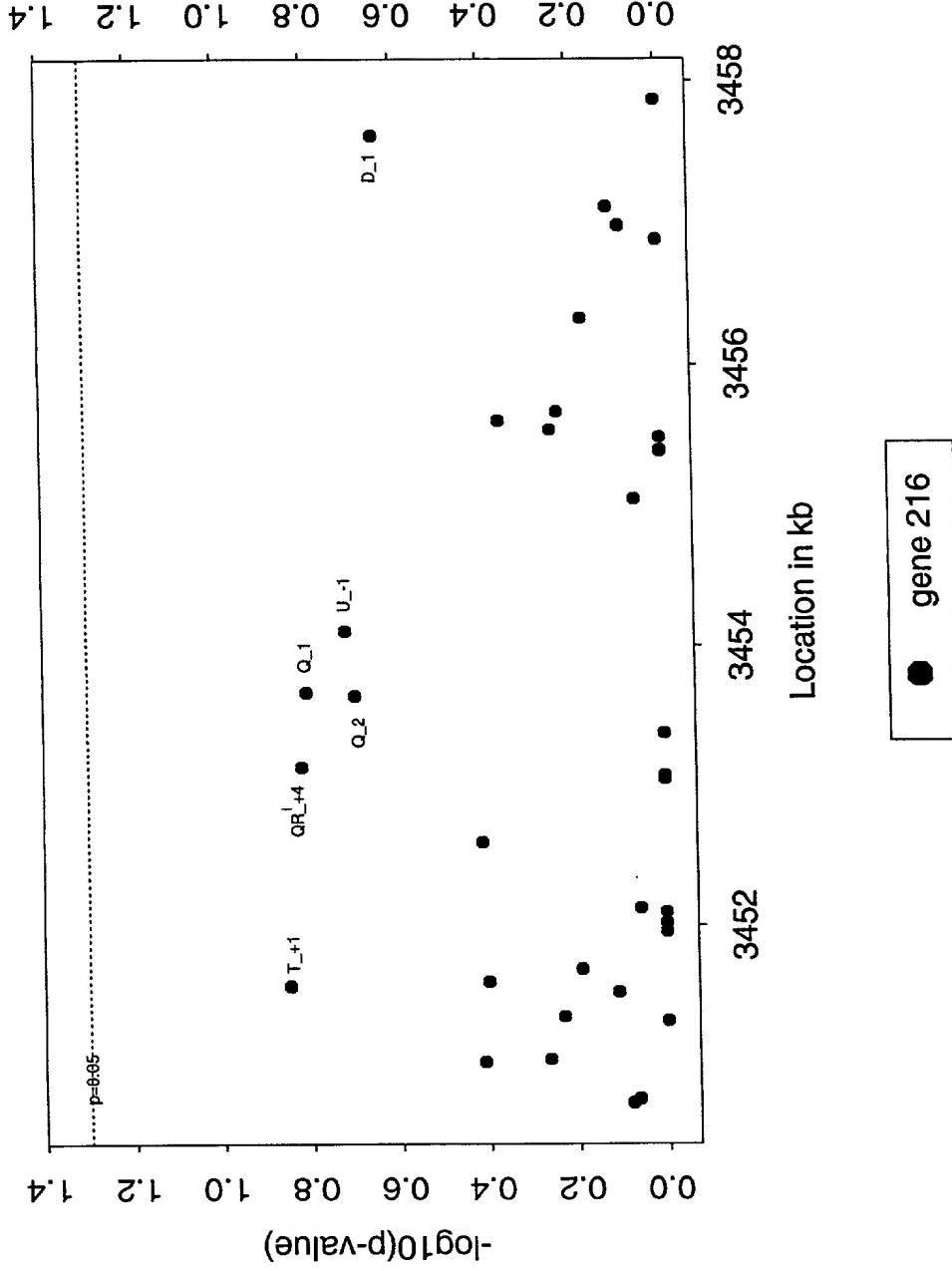
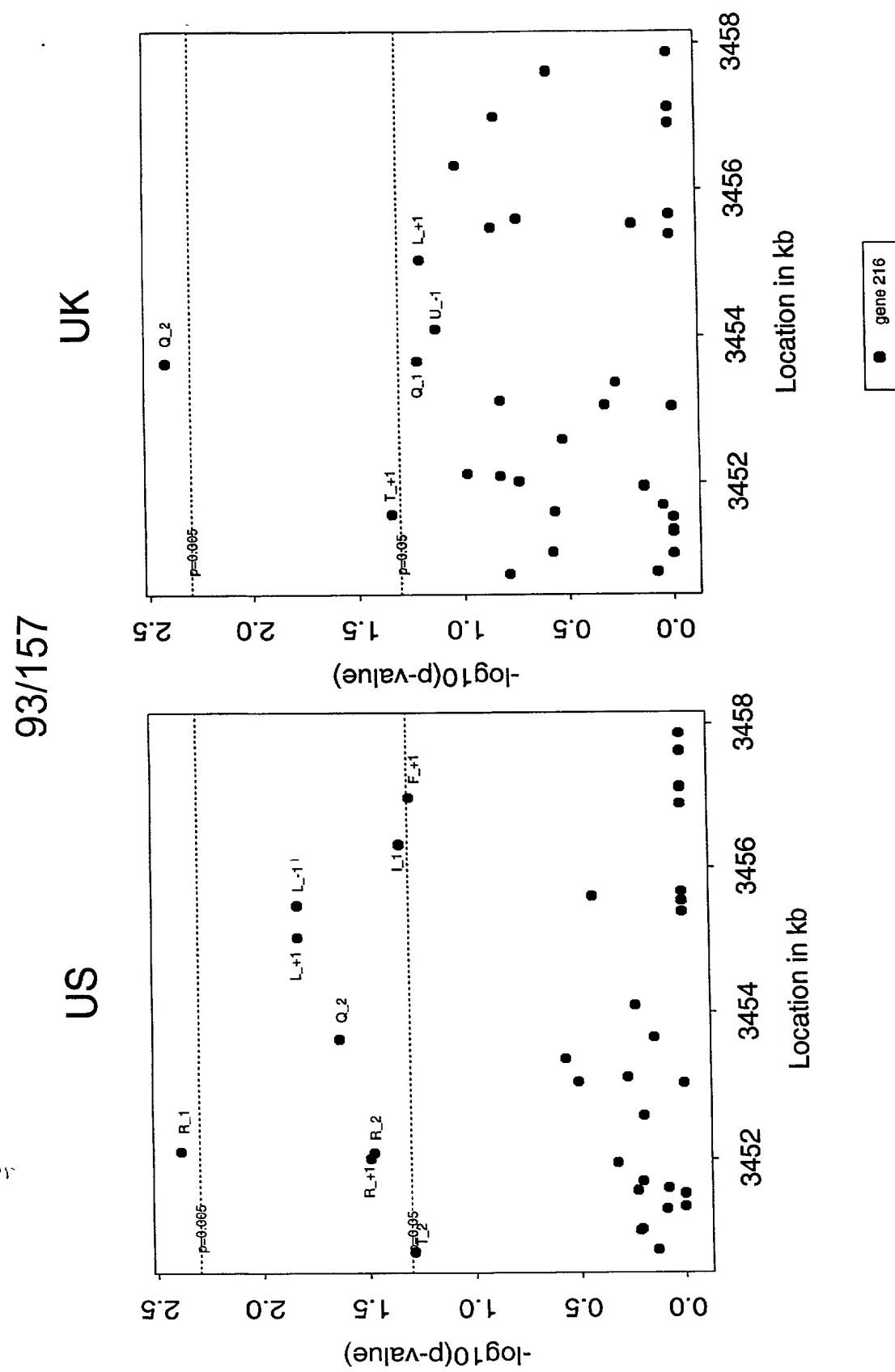


FIG. 27

FIG. 28



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10 30 50
CGCAACTGGAGTGAGTCTCTTCTTGCACCCAAACAGCTGGCTAGAACAGAGGAGTCA
-----+-----+-----+-----+-----+

70 90 110
CATGTTAGTGGGTTTATTCTTAGACACCACATCTGTAGGAGGGGCCAGGGCTGCAAGTT
-----+-----+-----+-----+-----+-----+

130 150 170
ACATGACATTATCACAAATTACCTTACGCTGAAGTGATTGTGTCCTTCTGCTCCTT
-----+-----+-----+-----+-----+

190 210 230
GAGGCTTCGTGTGTTGCTCACATTGCCACCCACAATGACCAGCCCCGTGCATGGCACGC
-----+-----+-----+-----+-----+

250 270 290
AGTAGGTGGGCACGTGAACTAAGCGTTGTCTTGCTACATTGCTGACAGTGGGAGGGT
-----+-----+-----+-----+

310 330 350
GGAGAACATGGACTAAATCCAGAGGTGGACAGGGAGAGAGCAAGTCAAATGCAGCCAGA
-----+-----+-----+-----+

370 390 410
TGTTGGGGCTGTCTGGGAAGAGAGGGTAGGGAGGACCATAAGCAGCTGCTGAAGC
-----+-----+-----+-----+

430 450 470
TGCGGCTACTGGGGGATTTGGAATATCCGGCTTAGGAGTCTCACCTGCTCTGCATA
-----+-----+-----+-----+-----+

490 510 530
CTTCCAAGGGACATATGTCCATCTGGATTGGAGGCTCTCAGAGGGTTAGTTGTGTCC
-----+-----+-----+-----+-----+

550 570 590

FIG. 29

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GCTTCCAGTGGTCTGAGGCCTCCTGAGACTTTGTACATTCAATTAAAGTGTAAACATAC
-----+-----+-----+-----+-----+-----+

610 630 650
AGAAAAGTTCACACATTATAAATGCAACTCAAGGACTTTCCAAAAGCGAACACACCCAG
-----+-----+-----+-----+-----+

670 690 710
ATCAAGAAAATAGACCATCCTACAGTCCCCCCTTACACTCTGTACCAGTTGCAGCCCCAC
-----+-----+-----+-----+-----+

730 750 770
AAGGGTAACTACTGTCTTGACTTCGAACACCATAGATTGATTGCCTGTTTAAACTT
-----+-----+-----+-----+-----+

790 810 830
TACATAAGTAGAATCACAGAGTGTACAATGACTTGGAAAATGTTGACAATATCTA
-----+-----+-----+-----+-----+

850 870 890
TTAAAGCTAAAATACCCTTGCCTATGAACCTGAAATTCCACCCACCTGCCAAGGGACA
-----+-----+-----+-----+-----+

910 930 950
AAAAGTTCCCTCTAAATGCACCAGGCTGTCAAGGATGAAGCGTTGGCTTGGGGCCCC
-----+-----+-----+-----+-----+

970 990 1010
ATTCACACACATGACCTTCTGGGCACCCAAGCATTAGCCTGTCGTACCAAGGTGCCA
-----+-----+-----+-----+-----+

1030 1050 1070
CCCTGGCGATCTCTGAAGGCTGGAGTCGGAGTGCCTCCCTCAGACATCCTGTCGTACCA
-----+-----+-----+-----+-----+

1090 1110 1130
ACTCCTTGGGAGAAGTCGTGTTACAGATGGTGGGTGTCAACCATGCCAAGCACTTCTAA
-----+-----+-----+-----+-----+

FIG. 29

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1150 1170 1190
GGGTTAACATGCTCACTGGTTGCCTGGTCCCAGGACATTCCCTGATGCCCTCTGGAGGG
-----+-----+-----+-----+-----+

1210 1230 1250
TGACGCCAACAGCCAGTGGAGAAGCCATCTTCCAGGTGCTGTCAGGCGCCCCGGAG
-----+-----+-----+-----+-----+-----+

1270 1290 1310
CTGCTCGGTGCATCCTAGGATCCCTCTCCTCAGCTTGGTTGATGGCCTCATCTCCTC
-----+-----+-----+-----+-----+-----+

1330 1350 1370
CCCTGCAACCTAAAATGTAATAAAACCCTTCTCAGAGACTTCGGCAGAAAATCCTCT
-----+-----+-----+-----+-----+

1390 1410 1430
GACCTGCACCTGGACACAGCTCATCTGGTTGGGAGGTGTCAACTGTGTAAAGGATGACT
-----+-----+-----+-----+

1450 1470 1490
CTGATCCCCATGTGGCTTTCGACTGTGTCCCTCTACAGTCAGTTATTAGCACTGACTG
-----+-----+-----+-----+-----+

1510 1530 1550
TGCTAGGAAGTGAGCAACACACATATTCCAGACCACATGGAGCTCAGGAGCTGGGAG
-----+-----+-----+-----+

1570 1590 1610
AGAGACAGGAAAGTGGACGACTACAGGGCCTCTGAAACGTGTTGCAGGGAGAAAGTGTCA
-----+-----+-----+-----+

1630 1650 1670
GTCAGGGGATGCTAACCTGGCTTGGTAAGGGACAGCCTCTGAATGACAGGACATTAAC
-----+-----+-----+-----+

1690 1710 1730

FIG. 29

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-----+-----+-----+-----+-----+-----+-----+
1750 1770 1790
GAACGCCAGAGTAGCTCCTCGAGCTGCCTCTGTACCTGACATCCACACTGAAGGCCAGCC
-----+-----+-----+-----+-----+-----+
1810 1830 1850
CCTCTGTGTTAGCCTTGCTTACTGAAGAGGTGTCGCTGAGGGGCTGCTCTGGGTGCT
-----+-----+-----+-----+-----+
1870 1890 1910
GCTCTGCTTCCTGTCCCCAACTTGTCTGAGCTCGAGCCACCTCCATACTGGTGCTCCT
-----+-----+-----+-----+-----+
1930 1950 1970
GGTTCTCAGGCCTTGAACTCAAACCTGAATCACACCACTGGCTTCCTCGTTCTCCAGCT
-----+-----+-----+-----+-----+
1990 2010 2030
TGCAGATGGCAGATTGGAACTTTTGGCCTCCATAATCACGTGAGCCAATTGCTATAA
-----+-----+-----+-----+-----+
2050 2070 2090
TAAATATCTCTCCCTCTTCTTCTCTCTGTGCAAATATAGTTCCAATTA
-----+-----+-----+-----+-----+
2110 2130 2150
TAAGAGCCCCTAAGGAAAATAACCCATGGTGCAGTGGTGAAGTAGAGAAACTGTGGTT
-----+-----+-----+-----+-----+
2170 2190 2210
CCCTCAAACCAACCGAACACTATTCAAGCAATCGAAGGAACAAACTATTGATATGCAAAT
-----+-----+-----+-----+-----+
2230 2250 2270
AGTGTAAATGAATCTAAAAACATCGGAAAGAGGGAAGGAAGCCAGACACAGAAGAGTGC
-----+-----+-----+-----+-----+

FIG. 29

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2290 2310 2330
ATGCCGCATGATTCCATTATGAAATTCTAGAACAGGCAAAACTTATCTATAGACAGA
-----+-----+-----+-----+-----+-----+

2350 2370 2390
GAACAAACAGATCAGTGGCTGTCTGGGTTGGGAGTGGGAAGTTGGCTGGAAGGGCACA
-----+-----+-----+-----+-----+-----+

2410 2430 2450
GGGCTCTTCTGTGAGTGAGGGAAATGTGTCTGCATTATAAGTGTGCTTATGTAGTTATAT
-----+-----+-----+-----+-----+-----+

2470 2490 2510
ACACTTATCGAAACTCATCTTAAGTGGCCACTAAAATAAGTCATTATTGTGTGTAAA
-----+-----+-----+-----+-----+

2530 2550 2570
TTATACCTTAATGAAGTTGATTGAAAATCAAAGTAGTAATAATAAGTAATAATCTCGT
-----+-----+-----+-----+-----+

2590 2610 2630
AGCTGGACAGCTGTGGTGAUTCACTCCTGTAATTCCAGCGATTTGAGAAGCTGAGGCAGG
-----+-----+-----+-----+-----+

2650 2670 2690
AGGATCACTTAAGATCAGGAGTTCTTTTATTTTATTTTATTTTGAGACGGAGTT
-----+-----+-----+-----+-----+

2710 2730 2750
CGCTCTTGTGCCAGGCTGGAGTGCAATGGCATGATCTGGCTCGCTGCAACCTCCACC
-----+-----+-----+-----+-----+

2770 2790 2810
TTCTGAGTTCAAGCGATTTCTGCCTCAGCCTCCAAAGTAGCTGGAACACTACAGGCGCTC
-----+-----+-----+-----+-----+

2830 2850 2870

FIG. 29

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ACCAACCATGCCGGCTAATTTGTATTTTAGAGAGATGGGGTTCACCATGTTGCC
-----+-----+-----+-----+-----+-----+

2890

2910

2930

AGACTGGTCTTGAACTCCTGACCTCCAGTGATCTGCCGCCCTCGGCCTCCAAAGTGCTG
-----+-----+-----+-----+-----+-----+

2950

2970

2990

GGATTACAGGCATGAGACACTGCGCCTGGCCAAGACCAGGGAGTTGAGACCAGCCTGGGA
-----+-----+-----+-----+-----+-----+

3010

3030

3050

AACAAAGTGAGACCCCTGTCTACAGAAAAATTAAAATTTAGCTGGGCCTGGTGCCTG
-----+-----+-----+-----+-----+-----+

3070

3090

3110

GTGCCTGTAGTTCCAGCTACTCAGGAGGCTGAGGTGGGAGGATACCTTGAGCCCAGGATT
-----+-----+-----+-----+-----+-----+

3130

3150

3170

TCAAGGCTGCAATGAGGCATGATCAGGCCACTGTCCTCTAGCGTGGGTGACAGAGTGAGA
-----+-----+-----+-----+-----+-----+

3190

3210

3230

CCCTGTCTAAATAATAATCATAAGAACACAAGGACCCCTAAACGCACTGATATCTA
-----+-----+-----+-----+-----+-----+

3250

3270

3290

AGGTGTATTAAGCGACCAAAAAAAAAAGAAAATCAAAGTGCAGAAAAACGTTAATAAGA
-----+-----+-----+-----+-----+-----+

3310

3330

3350

GAAAAAAATATGTCTGTATTGTCTTGAGTGAGGAAAAATAATCTAAAGCCTATGAAAGA
-----+-----+-----+-----+-----+-----+

3370

3390

3410

AACTAATCATATTGGTTCTGTTGGTGAGGGAGGGCTAAGAGCACGGAGACTTTCCCTA
-----+-----+-----+-----+-----+-----+

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3430 3450 3470
TGCTTCTGTACTTTGAGATATGTGAATGTAGTTCTCTCACTGCTCGAAC
-----+-----+-----+-----+-----+

3490 3510 3530
TTTCACTAACCAAATTACTACATTCAAATTCTCAAAACAAATAGATTACTAAAAGT
-----+-----+-----+-----+-----+

3550 3570 3590
AGGCTGGGTGCGGTGTCTCACGCCTGTAATTCCAGCGCTTGGGAGGCCGAGGCCAG
-----+-----+-----+-----+-----+

3610 3630 3650
ATCACCTGAGGTGGGAGTTCGAGACCAGCCTGACCAACATGGAGAAACCCATCTAC
-----+-----+-----+-----+-----+

3670 3690 3710
TAAAAATACAAAATTAGCCAGGCGTGGTGGCGAATGCCTGTAATGCCAGCTACTCGGAG
-----+-----+-----+-----+-----+

3730 3750 3770
GCTGAGGCAGAAGAACACTTGAATCTGGGAGGCAGAGGTTGCAGTGAGCCCAGATCATG
-----+-----+-----+-----+-----+

3790 3810 3830
CCATTGCACCTCCAGTCTGGTAACAAGAGAGAACTCTGTCTCAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+

3850 3870 3890
AAAAGATTGCTTAAAGTTAACATCTCCGGCCGGCGCGGTGGCTCATGCCTGTAATCC
-----+-----+-----+-----+-----+

3910 3930 3950
CAGCGCTTGAGAGGCCGAGGCAGGTGGATCACGAGATCAGGAGATTGAGACCATCCTGG
-----+-----+-----+-----+

3970 3990 4010

FIG. 29

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CCAAAATGGTGAACCTCGTCTGCTAAAAATACAAAAGTTAGCTGGGGTAGCGC
-----+-----+-----+-----+-----+-----+

4030 4050 4070
GCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGT
-----+-----+-----+-----+-----+-----+

4090 4110 4130
CGGAGGTTGCAGTGAGCCAAGATCGCGCGCTGCACTCCAGCCTGGCGACAGAGGGAGAC
-----+-----+-----+-----+-----+-----+

4150 4170 4190
TCCATCTCAAAAAAAAAAAAAAAAGTTAACATCTCATCCAAATTGCACCGAGTA
-----+-----+-----+-----+-----+-----+

4210 4230 4250
GGAAAACAAAAGTTAAAACATGAAACAGATGTTACTGAGGCCAAGGGTCTCCCAGGC
-----+-----+-----+-----+-----+-----+

4270 4290 4310
CTGGGAGTCAGCTTATGCAATTCTGCCCTCTGCCACCGCAGGGAAAGAAAGGTT
-----+-----+-----+-----+-----+-----+

4330 4350 4370
GTCTCCGTCTGCATGCCCTTGCCAGCAATGAAGCCCCAAGACAGCGGCAGCCGG
-----+-----+-----+-----+-----+-----+

4390 4410 4430
TTGCCTGAACCTCCTATCCTGGGGCACCCAGTGCAGGTGGATGACCCGACTAACCT
-----+-----+-----+-----+-----+-----+

4450 4470 4490
CGGCCAGGGCACCCCTGGGGCAGGACGGTAGCAAGGAGGGACAGAGATGGCCCCAGG
-----+-----+-----+-----+-----+-----+

4510 4530 4550
AGACCACGGAAGATCGCGCTCCTGGGGCAACTTCAGCAGCGAGAGGCGGCTTGCCCA
-----+-----+-----+-----+-----+-----+

FIG. 29

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4570 4590 4610
CCGCCTCATCCCACCACGCCCGGGCCTCCAAGAACCTTCCCAGCGTTCTCTCCTCCTC
-----+-----+-----+-----+-----+

4630 4650 4670
TCAGGAGTAGAGGCCCTTGAGACCGACGGGAGGGACGGCTGGGCCGGTCATCCGAGG
-----+-----+-----+-----+-----+

4690 4710 4730
GCCCGCACGGATTCCCTCCGCCAGCTCCACCCCTCGAGGGCGGCGGTCCGGGAG
-----+-----+-----+-----+-----+

4750 4770 4790
TGGCGACCCGGCTCCCCATGGCGCGCGCGTCGGGCCCCCTGGCCAGGCTCCGAGCGGG
-----+-----+-----+-----+-----+

4810 4830 4850
GTGGCGGGGAGGGGAGGCAGCGAGGGCGGGCGGTGGAGGTGGGGCGGGAAAGGTC
-----+-----+-----+-----+-----+

4870 4890 4910
CGAAGGCGGCGGCCTGAGGCTGCACCGGGCACGGTCGGCCGAATCCAGCCTGGCGGA
-----+-----+-----+-----+-----+

4930 4950 4970
GCCGGAGTTGCGAGCCGCTGCCTAGAGGCCAGGGAGCTCACAGCTATGGCTGGAGGCC
-----+-----+-----+-----+-----+

4990 5010 5030
CGGAGAGCTGGGGACCCGTTGCTGCTGCTACTACTGCTGCTGCTGGCCAGTG
-----+-----+-----+-----+-----+

5050 5070 5090
CCAGGCGCCGGGTGCTCAAGGTGAGGACGCCGGCGGGTGCGCCCTGAGGGCAGGCT
-----+-----+-----+-----+-----+

5110 5130 5150

FIG. 29

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AGGCACGGTGGTGGATGGGTTCTGCTCAGAGCTCGGTCAAGCGCGGAGGG
-----+-----+-----+-----+-----+-----+

5170 5190 5210

TCTCACGGCCCGGCACCATACGCCAGTAGGTCAAGGGCTGGGACTCTTGCCCCGT
-----+-----+-----+-----+-----+-----+-----+

5230 5250 5270

CTCCGTGGGACCTGCCAGGGACGCTCAAGTGTGCTTGGCTGGCCCCGGGACTT
-----+-----+-----+-----+-----+-----+-----+

5290 5310 5330

GCCCACACTGCCGGCTGCCACTCCGCTGGCAAAGCAGAGGCATGGCTCCCTCCCCCTC
-----+-----+-----+-----+-----+-----+-----+

5350 5370 5390

GGGACAGCCCAGCCCCAGCCCCAGGCCATAGCGTAGCCCCCTGCCTGGATTCTC
-----+-----+-----+-----+-----+-----+-----+

5410 5430 5450

GCTCTCACACCAGCTCCATCCGAGGCCACCGTGTGACCCGCTCTGCTCCACCC
-----+-----+-----+-----+-----+-----+-----+

5470 5490 5510

CTTAGGACTCAGCGGGCTCCATCCTCTAGGAAGCCCCATGCCAAGAGTCCCCAGAG
-----+-----+-----+-----+-----+-----+-----+

5530 5550 5570

TCCCTGCTTGTCTCAGGCTGCAGAACTAGCTGTGGCTCCACCCCTGCTCACCCCTCGT
-----+-----+-----+-----+-----+-----+-----+

5590 5610 5630

CCCTCCTCCCAGGGCAGCAGGGCAGTGTATGTTATATTGTTGCCTGTTGGT
-----+-----+-----+-----+-----+-----+-----+

5650 5670 5690

AGATAGAGAACGGCCCTCCAGATAGAACGGTGTCTGTTAGCAGTGCTCTGAAAGACTG
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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5710 5730 5750
CAGCTGTCTCCTCGGGTAACCCCTCAAACAAAGATGTTAAGATGGGCTGGAACAACC
-----+-----+-----+-----+-----+-----+

5770 5790 5810
TCTGCAAGCGGGTGGGAGGATTAGCCAGTCCTGCACAGCAAGTGCCTGGCCGGAACAGG
-----+-----+-----+-----+-----+-----+

5830 5850 5870
GAGGGCAACCAGGGAGGGGGCATGCGGGCTGGGCTGTGCTATGCAGACTGGCGGTGGC
-----+-----+-----+-----+-----+-----+

5890 5910 5930
TTCCACAGCACTGTGTGGGACCAAACAGGTACAGGGCCTGGTCTGTTCTGGCCCCAGG
-----+-----+-----+-----+-----+-----+

5950 5970 5990
GGAGGGCCCCAGGCGGTCCACTGCTCCCTCCCCTCTGAGCCCTATCCTGGGTCAGGGGA
-----+-----+-----+-----+-----+-----+

6010 6030 6050
GGTGATGGGACCCCTGGGAGAGGGCGTCTATGTGCCAATACCAGCCTGGCTCCCTCGG
-----+-----+-----+-----+-----+-----+

6070 6090 6110
GTTCCACCCCCATTCACCGGTACCGGAGCTCCAGCTCCAGCTCAGCTCTGCCCTCT
-----+-----+-----+-----+-----+-----+

6130 6150 6170
CTCCCTCATGGGTCAGGTGCCCGTGGCCAGCACGTGCGCGCAAGGCCATGTGGACAG
-----+-----+-----+-----+-----+-----+

6190 6210 6230
CACCCACACACCAACTGCACCCACACCACACCTGTGCCCGGCCACCTACCTCTCC
-----+-----+-----+-----+-----+-----+

6250 6270 6290
-----+-----+-----+-----+-----+-----+

FIG. 29

CCAAACCCTTAGAGGCCTAGGAGCAGCAAAGCTTGGTTCTACTCTCAGTTAAGTGCTC
 -----+-----+-----+-----+-----+

6310	6330	6350
------	------	------

TCTGGGCTGAGAGACCTCCCCTCCTCCCCACATCCACTCAGAGCCCTCCCTGC
 -----+-----+-----+-----+

6370	6390	6410
------	------	------

ACTGGCCCTCTAGCCTCTTCCAAGGTGGCAGACTCCTCTCGGCCCTCATCTGCCTGA
 -----+-----+-----+-----+

6430	6450	6470
------	------	------

TGGCAATTCACTCATCCAATCAAGGAGGGCTTCTGGAGGAAGGGTCTTGATGTTGTA
 -----+-----+-----+-----+

6490	6510	6530
------	------	------

GTCTGGGAGAGAAGGTGGAGGAGAAAAAAAGGAGTTGGGTGGCCTAGCAGGAGCTGAGTC
 -----+-----+-----+-----+

6550	6570	6590
------	------	------

ACTTCCACAGGCAGCCATCAGCCCAGCAGGACTGAGGCCAGGGCTGCGTGGAGGGGGAG
 -----+-----+-----+-----+

6610	6630	6650
------	------	------

GCTGTCTGTCTGGGAGCTGGACTGGTACCGGGGAAGGAGGGCTGCTGCAGGCTCTG
 -----+-----+-----+-----+

6670	6690	6710
------	------	------

GGTGCCTGGGCCTGGCTCCTGCAGGGCGGCCCTGTGAGAGTGGTTGGGCCAGTGGAGG
 -----+-----+-----+-----+

6730	6750	6770
------	------	------

GGCTGGAGCATTCCAGGGAACATTCCAGGCGCCCTCTGAGTAATGCTTGGCTCTGGGA
 -----+-----+-----+-----+

6790	6810	6830
------	------	------

TTCCTCCTAGAGCCCCCTTAGGCACACCCGCCAGGGAGCACCAAGGCTCCGTCCGGAAAG
 -----+-----+-----+-----+

FIG. 29

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6850 6870 6890
CGTCCCCTCCCTTGAAAGAGATGAGGAGGGCCTCTGGGCCAGGGTACCAAAACCCTGC
-----+-----+-----+-----+-----+

6910 6930 6950
CACCAAGGACAGAGTCCCCGAGGGAGCTCTGGCAAGGTGGACCTCGCAAGGCAACATCTG
-----+-----+-----+-----+-----+

6970 6990 7010
GCTGTTGTTTCTCAGATGATGGGGGGGGCACAAGTGTCTCTTCGTACATCTCTCA
-----+-----+-----+-----+-----+

7030 7050 7070
CCCTAAAGGCATCTGCTGCCATCTAAAATCCCTAAGGCTGCCCGCTTTCCCTCCC
-----+-----+-----+-----+-----+

7090 7110 7130
CTCTGCACTGGCGGCCTTGGCTCTTCCCTGTGATGCCGAGCCAAAGCCTGCCCGA
-----+-----+-----+-----+-----+

7150 7170 7190
CAAAGGTCAGGGACTCCGTGTCCCCAGCTGAGCTGTCCTTCCAGCCTCTTTTC
-----+-----+-----+-----+-----+

7210 7230 7250
CTCCTCCTGATAGCTCCTCAGATCCAAGGATGCCACGGCGTCCCTCCTCCAGGC
-----+-----+-----+-----+-----+

7270 7290 7310
TGAGCCCACCGCGTGTGAAGGTGAAGTCTGCCCTAAAGGCCTCCAGTGCCTCCCTGGGG
-----+-----+-----+-----+-----+

7330 7350 7370
ATGTCCCTCTACCCCCCTCCCTGTCTTGTCCCATGCCCTGTGTTCCCTCAGGTCCCCCT
-----+-----+-----+-----+-----+

7390 7410 7430

FIG. 29

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CACCCCTGTGCTCTGTCTTACTCCAGGACATATCCCTGGCAGCCAGTCACCCCGCACTG
-----+-----+-----+-----+-----+-----+

7450

7470

7490

GGTCCTGGATGGACAACCCTGGCGACCGTCAGCCTGGAGGAGCCGGTCAGTGCCATGTC
-----+-----+-----+-----+-----+-----+

7510

7530

7550

TCCCCGCCCTCCACAGGGGCCCTGAACCTCCCAGCCCTTGTCTCCCTACATTACAG
-----+-----+-----+-----+-----+-----+

7570

7590

7610

CTTCTAGTTTGCTGGGTCCCCAGAACCAAGTCACTACTCCTATAGGCCCTGCCT
-----+-----+-----+-----+-----+-----+

7630

7650

7670

CCCCCTGCCCTCAAGTGGCAGAAGAAGGCAGTGGGTTGGACATCTGGATCTCGTGAG
-----+-----+-----+-----+-----+-----+

7690

7710

7730

CCCGCACACATGGAACTCATTTCAGCTTCTCCACCCCACCTCCCTTTCCCTCCCTCC
-----+-----+-----+-----+-----+-----+

7750

7770

7790

CTGGATGATCTGGCCACCCCCACCCCAACCAGGCAGAAATGGGTCCAGAGTTGTGGGT
-----+-----+-----+-----+-----+-----+

7810

7830

7850

CCTGAAGCTTTCAAGGAGCCTCTAAAAAAAAAAAAAAAAGCACCAAAAGAAAA
-----+-----+-----+-----+-----+-----+

7870

7890

7910

CCTTTGCAAAGTTGACCAGAACATGTGACCCCTGTGGACACACTGCTGTCCCTCTCAGGG
-----+-----+-----+-----+-----+-----+

7930

7950

7970

CCCTGCCACGAAGGCCTGAACCTTCAGCCTCACTGGCTCCTGTGGAATCCACTTCTGGTA
-----+-----+-----+-----+-----+-----+

FIG. 29

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7990

8010

8030

TGGGGGGGGCAGTGGTCACTCTCCTGATGTCCCCAGATGTAAGACCACCCATGTGCTT
-----+-----+-----+-----+-----+

8050

8070

8090

CTTCTGCAGGACGCTCTGCCCGCCCTTCCAATCCGCTTTCACACGCTTCCAGAA
-----+-----+-----+-----+-----+

8110

8130

8150

TAACCATGCCCATCTGTTGTGCCATAATATCTGTGCTGCAAACTAAGAGGGCAGTAGC
-----+-----+-----+-----+-----+

8170

8190

8210

CTTGATATGCTCATTTACAGAGGGCAAACGGAAGCCCAGAGAGCTGGGGAAATTGTC
-----+-----+-----+-----+-----+

8230

8250

8270

CATGGTCACACAGCTTTAGGCTGGGAGCCTGAGACCCACTAAGGTCTGAACGATTTA
-----+-----+-----+-----+-----+

8290

8310

8330

AACCATTGGCTACACCCCTGCCCTCTAGAGAGCCCTTTGTTGGAATTTCAAGCCC
-----+-----+-----+-----+-----+

8350

8370

8390

TACTGTCCAATCCAGCAAGAGGGAAAGGCAGGGAGCATTGCCATGAAGGCTGAGAGGCC
-----+-----+-----+-----+-----+

8410

8430

8450

CCCAGAGACCCAGCAGCTCCAAACCCAGGGCCCTCACTGGGATCCCTAGGCCATAAGG
-----+-----+-----+-----+-----+

8470

8490

8510

CCCCCATTCCACTGGTCAAGCACGGCACTGCCCTGAGCTTGAGATTGCCCTCCCCATCC
-----+-----+-----+-----+-----+

8530

8550

8570

FIG. 29

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CCAGGAGGGAAAGGCTGGACACACACTGGGGTCACTCTGCCTCTGGCCTCCGTCTGT
-----+-----+-----+-----+-----+
8590 8610 8630
CTGGCCTGGGTGTGACCAAGAGGGAGGCCAAAGGGCTCTGCTCCCCACCGGTGG
-----+-----+-----+-----+-----+
8650 8670 8690
GCCCTGCCAGGAAGCCTGCCAAGATGGTACAGAAGAAAGAGTAGAGGCTAGGTATC
-----+-----+-----+-----+-----+
8710 8730 8750
CCCTCAAAGGCAGGAAACACTCACATTCAAGATGAGGGTATATATCAAGGGCAGG
-----+-----+-----+-----+-----+
8770 8790 8810
GTACCAGGAGGGCAAGAGTAAAGATAGCAGGGCTGCAGAGGAACAGGGACCTCGAGTAT
-----+-----+-----+-----+-----+
8830 8850 8870
GGCCTTTTCCCGGTGCAGACCTTCCCCAATAAGCAAGTGGCATTCCAGCCTCATGAG
-----+-----+-----+-----+-----+
8890 8910 8930
CTCATGCTGGAGGCCTTGTGGGCCTGTGGCAGGGAGGCAAGGACCATCTGCTCCCCAC
-----+-----+-----+-----+-----+
8950 8970 8990
TTGCGAAGGAAGAACTCCCTCCAAAGACTCTGAGACCCCTGGACAGGGCCCCAGGCCAGT
-----+-----+-----+-----+-----+
9010 9030 9050
GCATTTTGAGAAAAGGAGTCGGGGTTAACATTCCGAAGGCAGCAGCCTCCAGG
-----+-----+-----+-----+-----+
9070 9090 9110
AAGCTCCTGGCCGGCTCCAACCTGGGCCCCCAGCCAGGCTGAGTGGACAAGGGGAAG
-----+-----+-----+-----+-----+

FIG. 29

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9130 9150 9170
TGGGTGTTCCCACAGGGTGGAGACGCCAAGAGGGTGGGGAAGGAGAGAGGGCTGGCC
-----+-----+-----+-----+-----+-----+

9190 9210 9230
GTCCAAGCCAGCCTCCTGACACCTAGCTGAGAGCCAGTGTGCTCTTGGCTGGAATGGC
-----+-----+-----+-----+-----+-----+

9250 9270 9290
GTCCATGTTACTCGTGGTCCAGTGAAGCAGGTGTCGGAGCCGGAGGGACGGGGCTG
-----+-----+-----+-----+-----+-----+

9310 9330 9350
CTGGAGGCCAGGAAACTTGGAAGAGGGAGCAGTTGCCAAATTGGAAGTGGAGGAG
-----+-----+-----+-----+-----+-----+

9370 9390 9410
TCAAATTGAATTCTATAGGAAATGAGCAGCAGCTCATTTGGAACCAAGCCTCAGGTAGC
-----+-----+-----+-----+-----+-----+

9430 9450 9470
AGAGGCTCTGAGGAGGCCCTGACCATGGCTACCGATGCCCCATAATGTCCTCAGCAC
-----+-----+-----+-----+-----+-----+

9490 9510 9530
CCTCTGTCTCCCCCTGCTTTGATGCCCTCTGGCATGAAAGAAGAGGGCGGGCCAG
-----+-----+-----+-----+-----+-----+

9550 9570 9590
GGGAGGGCACCTTCTGGACCTCTGGTCTCTAGGGAGGATGCTGGTGTGCCCTGGCAGG
-----+-----+-----+-----+-----+-----+

9610 9630 9650
CTGTGCCAACGCCCTTCCAAGTGGCTGTTGTCAGGACTGCAAACATCCTGAGTTGGAA
-----+-----+-----+-----+-----+-----+

9670 9690 9710

FIG. 29

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CATCTTGTATGTTCTCACCTCCTCCACGCCCTCCATAGTATGGGGGGTCTGCTGAC
-----+-----+-----+-----+-----+-----+-----+-----+
9730 9750 9770
TCCCCAGCCCACGTTCTCCCCAAGAACTTCCTCCCCAGCCGGTCCACAGGCCACCTACT
-----+-----+-----+-----+-----+-----+-----+
9790 9810 9830
CCCTGGCAGGCAGGAGGCCTGGAGGCCACCATCTCAGCTCCACACTCTTTCTTGCCAGG
-----+-----+-----+-----+-----+-----+
9850 9870 9890
TCTCGAACGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTG
-----+-----+-----+-----+-----+-----+
9910 9930 9950
AGCTGGAGAAGAACCACTGAGTGCCAGGCTGGGTAGGGCTGGAGGAGGGATCAGTGT
-----+-----+-----+-----+-----+
9970 9990 10010
TGGGGGGCAGGGACTGACACAGATCTGTGCGGGTGGCTGGATGGCAGAGGACCCAGAG
-----+-----+-----+-----+-----+
10030 10050 10070
AGGGTGCAGATGACAGGGAGAGTCACGCAGGCCTGTGGTTGGCTCCCTGGAGGCTGAAGA
-----+-----+-----+-----+-----+
10090 10110 10130
GGACCGCTGAGGCTGTCAGCCCCGCTGTGGGCACCTCCGCCCTCCCAACCCAGGAGCG
-----+-----+-----+-----+-----+
10150 10170 10190
GCTTGTAGCTCCCTGCTGGCGATGAGTGAGCACCACCTAGTGGACATTGCAAGATATG
-----+-----+-----+-----+-----+
10210 10230 10250
CTGAGTCTAAAGAAATCCTAGAGGGAAAAGATGAGGCCGGCACCCAGGCTAAGGGAATGG
-----+-----+-----+-----+-----+

FIG. 29

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10270 10290 10310
CAGGGACCAAGATGCGGTGGCTTGGGAGGCCAGGCAGGCGGCTCACCTGAGGTAGGA
-----+-----+-----+-----+-----+-----+

10330 10350 10370
GTTTGAGACCAGCCTGCCAACATGGTGAAACCCCGTCTACTAAAAATACAAAAAATT
-----+-----+-----+-----+-----+-----+

10390 10410 10430
AGCCAGGCCTGGTGGCGCGCCTGTAATCCCAGCTACTTAGGGGCTGAGACGGGAGAAT
-----+-----+-----+-----+-----+-----+

10450 10470 10490
CGCTTGAACCCGGAGGTAGAGGTTGTGGTGAGCCAAGATCACACCACTGCACCACTCCG
-----+-----+-----+-----+-----+-----+-----+

10510 10530 10550
GCCTGGCAAAGAGTGAGACTCCGTCTCAAAAAAGAGAAAAAGAAAAAGAAAAAAA
-----+-----+-----+-----+-----+-----+-----+

10570 10590 10610
AAAAGAAAGAAAAGAAAAAGAAAAAGATGCAGTGGCTACACTGGGGCAGCAGTTGT
-----+-----+-----+-----+-----+-----+-----+

10630 10650 10670
CTGACCTGCCTGGAAGGTCTCCATCTACAGGGAGGGAGCAGGGGGAAATGAATTGGAG
-----+-----+-----+-----+-----+-----+

10690 10710 10730
AGTCCCAGGAGGCCAGATCACAGAAGGCCATTTGGTGCTCAGTGTCCCTGGACCATCCA
-----+-----+-----+-----+-----+-----+-----+

10750 10770 10790
GAGCCAAAGATTTGAGCTGGGAAGGGACAGGCAGACCTGTGCTCAGGAAGGTGCCTTG
-----+-----+-----+-----+-----+-----+-----+

10810 10830 10850

FIG. 29

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GGCTGGGTGGGTGGGTGTCGGGCTGGAGCGCAGGCTTAAAACCACCCAGATTATGT
-----+-----+-----+-----+-----+-----+

10870 10890 10910

TATCAGTATATATCACCTACTGAGTGCTTGACCGCAGGCCTGTTCTGAGCACTTGACAC
-----+-----+-----+-----+-----+-----+

10930 10950 10970

GTATTTATTCTCCCTCGTGGAGTCGGATGGACAGGGAACAAACTCTAGTTCCACTGTGC
-----+-----+-----+-----+-----+-----+

10990 11010 11030

CCAACCATAAATCCCACGTCCCTACCCCTTCAATGGGTGGTCACATCACCTACCTCC
-----+-----+-----+-----+-----+-----+

11050 11070 11090

TAGGGTGGCGGGTGTGTGGGGCAGGGTAGGGGGCAGAGCTGGGCAGGTGGTGGAAAT
-----+-----+-----+-----+-----+-----+

11110 11130 11150

GCCTGGGAGGGGGAAGCAGCCATCATTAGCGGGTGGTCTGGAGGTAATGAGGCCAAGGT
-----+-----+-----+-----+-----+-----+

11170 11190 11210

GAGGTTGGGTTAAGGATTTCTTAAAGAAGACAGATTGACTTATGATTGATCCATCCGT
-----+-----+-----+-----+-----+-----+

11230 11250 11270

GTGGGAAAGATCCTGTTGAGATGGAGCCTGAAGATGGAATCATTACCGGAGTGGTGTGG
-----+-----+-----+-----+-----+-----+

11290 11310 11330

AGAAGGCAGGGAGGGTGGAAAGCAGCGTGGCAGGTGGCATTCTGTTCTGGAGGCA
-----+-----+-----+-----+-----+-----+

11350 11370 11390

GGGGGTGAGCATCAACTGAAGGACAGGTGGAGGTATGTGGGTCTAGAAGTCTGAG
-----+-----+-----+-----+-----+-----+

FIG. 29

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11410 11430 11450
GAAAATATTCAAGGATCTAGGCAGGTGGGGCAAGAGGGTCGACCAGATGCCAACAA
-----+-----+-----+-----+-----+-----+

11470 11490 11510
AGGAGGGCAGCAGGCAGGGAACTGGGGAGGTACCGCATTCCCCACTCCAAGTCCC
-----+-----+-----+-----+-----+-----+

11530 11550 11570
ATTCTCGGCAGTGTCTCCTGACTCCTCCCTCCGATCCTGTGGATCCTGCTGCCTGCT
-----+-----+-----+-----+-----+-----+

11590 11610 11630
GCAGGTCCCTGGAACCAACAAACTCTCCCTATTCCACTCCTCCCCGGCGTCCTCCC
-----+-----+-----+-----+-----+-----+

11650 11670 11690
TGGTGCTTCCCATATTCACATCTCCACAACTAAGCCATCACCAAGGCTCCTCCTCTAG
-----+-----+-----+-----+-----+

11710 11730 11750
CCCCAAGAGTTCTGATCTGAGCAAGTCACCATTGCTCCTGTCCCTCCCTAACACACAC
-----+-----+-----+-----+-----+

11770 11790 11810
TGTGAGTGTCTCACTCATAAAGCTGCTCCATTAGCATTAGGGAGGAAGGCTGGGAGACA
-----+-----+-----+-----+-----+

11830 11850 11870
TCCTGGAGGAGGCAGGAGGAAGCTGAATTCAGTGTTCCCTGTAACACCCCCCTCAGCAG
-----+-----+-----+-----+-----+

11890 11910 11930
GCTGCTGGCCCCAGGATACATAGAAACCCACTACGGCCAGATGGCAGCCAGTGGTGCT
-----+-----+-----+-----+-----+

11950 11970 11990

FIG. 29

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GGCCCCAACCACACGGTGAGATGCTTCCATGGGCTCTGGGATGCACGCCAGAGGTACC
-----+-----+-----+-----+-----+-----+

12010 12030 12050
CCCCCACCATCCTACCCCTACTCCTCCTTGCAATTCTAAGGGCGTTGGAGCCAGCCC
-----+-----+-----+-----+-----+

12070 12090 12110
CTACCACACCCTCCCTCTTGCCCCCTTGCTCCAGCCCTGGCTGAGATTGGGCTGGCC
-----+-----+-----+-----+-----+

12130 12150 12170
CCTTCCTCCCTAGGATCATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTG
-----+-----+-----+-----+-----+

12190 12210 12230
GGTAGTCCTCTGCACCTGCTCTGGATGAGGTGAGCTCTGGAGAGGAGGCTGGCCTGG
-----+-----+-----+-----+-----+

12250 12270 12290
GATGGGAAAGAGCTCCCTCACACCCGCTCCTACCCCTCTGCACCCCTAGTGGCCTGATCA
-----+-----+-----+-----+-----+

12310 12330 12350
CCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCGGGCTCCAAGGACT
-----+-----+-----+-----+-----+

12370 12390 12410
TCTCAACCCACGAGATCTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCC
-----+-----+-----+-----+-----+

12430 12450 12470
ACAGGGATCCTGGAACAAAGCGGGCATGACCAGCCTCCTGGTGGTCCCCAGAGCAGGG
-----+-----+-----+-----+-----+

12490 12510 12530
TCAGGGGCATCGATCGATGGAGTGGGAATGCTGTATCTATAGCCCTCAAATCAGAAG
-----+-----+-----+-----+-----+

FIG. 29

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12550 12570 12590
AGACGGAATTCACAGGCCTCGAGTCCCAGTATTTTATTGAAGTCTGAAGAAACAAGTT
-----+-----+-----+-----+-----+

12610 12630 12650
CCAGAAAACATGTTAAACTTCCTCTGGGAGCTGGGGTTGGGGGTCAAGGGCTCAAGGCCA
-----+-----+-----+-----+-----+

12670 12690 12710
GCAGCTTCCACTCAGGGTCCCCATTGCACCTCCGCAGGGCAGGCAGAGAAGCGCGCAGGA
-----+-----+-----+-----+-----+

12730 12750 12770
CCCGGAAGTACCTGGAACGTACATTGTGGCAGACCACACCCTGGTGAGGAGAGACCCA
-----+-----+-----+-----+-----+

12790 12810 12830
GGGGTTGGGGGTCAAGGATGGGCCAGCTCAGCCCCCTAAGCCACCGGATTCTGCC
-----+-----+-----+-----+-----+

12850 12870 12890
TTCCCAGTTCTGACTCGCACCGAAACTGAACCAACACAAACAGCGTCTCTGGAAGT
-----+-----+-----+-----+-----+

12910 12930 12950
CGCCAACGTGGACCAGGTTGGGGCGGCGGGAGAGAGCGGTATGGGGTGGCGGC
-----+-----+-----+-----+-----+

12970 12990 13010
GGCAGGACAGGCAGGTGCTGGTGGGTTGGGAAGAGGAAGGGCGCCACGAAGGACC
-----+-----+-----+-----+-----+

13030 13050 13070
ACCGGGCGCATGGGGCGCCCTGTCGGCTCAGCCCCGCTCGCCCTCAGCTTCTCAGG
-----+-----+-----+-----+-----+

13090 13110 13130

FIG. 29

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ACTCTGGACATTCAAGGTGGCGCTGACCGCCCTGGAGGTGTGGACCGAGC
-----+-----+-----+-----+-----+-----+-----+
13150 13170 13190
CGCGTCACGCAGGACGCCAACGCCACGCTCTGGCCTTCCTGCAGTGGGCCGGGGGCTG
-----+-----+-----+-----+-----+-----+-----+
13210 13230 13250
TGGGCGCAGCGGCCACGACTCCGCGAGCTGCTCACGTGGGTGCCTCTGACCCGGACG
-----+-----+-----+-----+-----+-----+-----+
13270 13290 13310
CGGGTCCC GG GTGGGCGGCCCTCACCTCCCGCCCCGCCTGGTCACGCCGCGCTCCGCC
-----+-----+-----+-----+-----+-----+-----+
13330 13350 13370
CCAGGGGCCGCGCCTCCAGGGGCCACAGTGGCCTGGCGCCCGTCGAGGGCATGTGCG
-----+-----+-----+-----+-----+-----+-----+
13390 13410 13430
GCGCCGAGAGCTCGGGAGGGGTGAGCACGGTGAGCCCCGCGGGGGGGGAGGGAGAGA
-----+-----+-----+-----+-----+-----+-----+
13450 13470 13490
CAGGAGGCTCTACGGCCGCAGT GACC GCC CTCCACGGCCCCCAGGACC ACTCGGAGC
-----+-----+-----+-----+-----+-----+-----+
13510 13530 13550
CCCCATCGGCGCCGCAGCCACCATGGCCATGAGATCGGCCACAGCCTCGGCCTCAGCC
-----+-----+-----+-----+-----+-----+-----+
13570 13590 13610
CGACCCCGACGGCTGCTGGTGGAGGTGCGGCCAGTCCGGAGGCTGCGTCATGGCTG
-----+-----+-----+-----+-----+-----+-----+
13630 13650 13670
GGCCACCGGGTACGCCGGTGGGGGCTGGGGCTGCCGGGGCGGCTAGTCCTGGGGAC
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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13690

13710

13730

TCCTCCGCTCGTTCTTGGTCGCCCTCAGTTCTCTGTAAAATGGGATAATG
-----+-----+-----+-----+-----+

13750

13770

13790

ATCATAGTGTCCGCTTCAGGGTGGTTATGAGGCTAAAGGAAGAAGCTCAGGCAAAGT
-----+-----+-----+-----+-----+-----+

13810

13830

13850

GGATTCTAACGGTATGAAGATTATTTCCGAGTAACCTGGCGAGGTTACTCCTACACCG
-----+-----+-----+-----+-----+-----+

13870

13890

13910

GGAGGAGCACCGTCGGGTCGCGATTCCACCTGGTCCCAGGCTGCTCACTATTGGGCC
-----+-----+-----+-----+-----+-----+

13930

13950

13970

GCATCGTCCCTGTCCCGTTGTTGTGACTTGCGGGTTACTTCCCTCTGGC
-----+-----+-----+-----+-----+-----+

13990

14010

14030

TCTGCGCGTCTGGCGGCTGTAGCCAAGCCCAGGGTGGGATCAGAGAACGCGGGGTT
-----+-----+-----+-----+-----+-----+

14050

14070

14090

GGGGACTGTCCCTCCATGCCAATGCCCTCCCCGTGCGGTAGGCACCCGTTCCGC
-----+-----+-----+-----+-----+-----+

14110

14130

14150

GTGTTCAGGCCCTGCAGCCGCCAGCTGCGCGGCTTCTTCCGCAAGGGGGCGCGCT
-----+-----+-----+-----+-----+-----+

14170

14190

14210

TGCCTCTCCAATGCCCGGACCCGGACTCCGGTGCCGCCGGCTCTGCGGAACGGC
-----+-----+-----+-----+-----+-----+

14230

14250

14270

FIG. 29

TTCTGGAAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGGTTAAGTCGGCTCGCCCG
 -----+-----+-----+-----+-----+

14290 14310 14330
 GCCCCCCACTTGCCCTCTCCGCTCAGGTCTGGGGCGCTGCCCTCACCTGGGCCTTCTT
 -----+-----+-----+-----+-----+

14350 14370 14390
 GCCTTCTGGTCCCAGGAGTGCCGCGACCTCTGCTGCTTGCTCACAACTGCTCGCTGCG
 -----+-----+-----+-----+-----+

14410 14430 14450
 CCCGGGGGCCAGTGCGCCACGGGACTGCTGCGTGCCTGCCTGGTGGGCATGGAA
 -----+-----+-----+-----+-----+

14470 14490 14510
 GGTCAGGGTGAGGGTTCGGGAGCTTGGGAGGCCGGCTGTTGGCCTAGTTAATTGGT
 -----+-----+-----+-----+-----+

14530 14550 14570
 GCCCTCAGTTCCCCCGTTGGGTGCTGGCTGGTAGGCCTGGCTCCCCCAGCTCCGAG
 -----+-----+-----+-----+-----+

14590 14610 14630
 CCGCGCTCTCGGCATGGACCTCTCACTGCACGTGGCCTCTCTGCCTCCCCACCACCC
 -----+-----+-----+-----+-----+

14650 14670 14690
 GTCACCTGCCAGCTGAAGCCGGCTGGAGGCCGTGTGCCGCCAGGCCATGGGTGACTGTGA
 -----+-----+-----+-----+-----+

14710 14730 14750
 CCTCCCTGAGTTTGACGGCACCTCCCTCCACTGTCCCCAGACGTTACCTACTGGA
 -----+-----+-----+-----+-----+

14770 14790 14810
 CGGCTCACCTGTGCCAGGGCAGTGGCTACTGCTGGGATGGCGCATGTCCCCACGCTGGA
 -----+-----+-----+-----+-----+

FIG. 29

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14830 14850 14870
GCAGCAGTGCCAGCAGCTCTGGGGCCTGGTGAGAGGACACGAGCACCCCTGCACCCCTGC
-----+-----+-----+-----+-----+-----+-----+

14890 14910 14930
CCCCCATCCTCTGGTGGGCCAGTTTCTACTGTGGGAAGATGGCAGGGAAACTGAG
-----+-----+-----+-----+-----+-----+-----+

14950 14970 14990
GCCCGCTGAGCGCAGCCCTCTCCGAGCTGCCCTGGCCCAGCCTGGCCATGCTTCCTCAGGCT
-----+-----+-----+-----+-----+-----+

15010 15030 15050
CCCACCCAGCTCCGAGGCCTGTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAA
-----+-----+-----+-----+-----+

15070 15090 15110
ACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGTAGGGAGTGGAGC
-----+-----+-----+-----+

15130 15150 15170
TGAGTGGAGGGAGCAGAAGCTATGGAGTGGTTGGGAAGGGGGTACTGCAGCTGTTG
-----+-----+-----+-----+

15190 15210 15230
ACCCCCCTCTACTTCCTCCCCAGGGATGCCCTGTGTGGAGCTGCAGTGCCAGGGTGGAA
-----+-----+-----+-----+

15250 15270 15290
AAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGC
-----+-----+-----+-----+

15310 15330 15350
CAGGAAGTGAATTGTCGGGAGCCTGGCACTCCCCAGTGCCAGCTGGACCTGCTTGGC
-----+-----+-----+-----+

15370 15390 15410

FIG. 29

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CTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGAGCTCTGCCAACCG
-----+-----+-----+-----+-----+-----+

15430 15450 15470
ACCCCTCCTGCCGTTGAATCCCCCAGGCCAGTGTCCCCCTCACTGCCTGGTGCAGTC
-----+-----+-----+-----+-----+

15490 15510 15530
CCGTAGGTGTGCCAGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGC
-----+-----+-----+-----+

15550 15570 15590
CTGACTGCCTGCCACAGCCACGGGTGAGAGGCCGAGGAGTGGGGTGACCTGGGTTC
-----+-----+-----+-----+

15610 15630 15650
CTAATCCTACGTGACCCCTCTTCTCTGCAGGTTGCAATAGCAACCATAACTG
-----+-----+-----+-----+

15670 15690 15710
CCACTGTGCTCCAGGCTGGCTCCACCCTCTGTGACAAGCCAGGCTTGGTGGCAGCAT
-----+-----+-----+-----+

15730 15750 15770
GGACAGTGGCCCTGTGCAGGCTGAAAGTATGCCAGTGGGGCATGTGGCAGGAGCTGG
-----+-----+-----+-----+

15790 15810 15830
GGTGGTGCACCTGCTCAGGACTCAGGCCCTCCCCAATCCCCCAGACCATGACACC
-----+-----+-----+-----+

15850 15870 15890
TTCCTGCTGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGGGGCCCTGGCC
-----+-----+-----+-----+

15910 15930 15950
TGGTGTGCTACCGACTCCAGGAGCCCCTGAGCGATGCAGCTGGGCTGCAGAAGG
-----+-----+-----+-----+

15960 15980 16000
TGGTGTGCTACCGACTCCAGGAGCCCCTGAGCGATGCAGCTGGGCTGCAGAAGG
-----+-----+-----+-----+

FIG. 29

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15970 15990 16010
GACCCTGCGTCAGTGGGTAGGCTCCGAGCGCCTGTTCTGAGCCTACTCCTGCGGTTCT
-----+-----+-----+-----+-----+

16030 16050 16070
CCCTCCTCAGAGCTCTGCTGGGCTGTGGAGCTGGGCAGGCCCTCAGCCTTGCCCCA
-----+-----+-----+-----+-----+

16090 16110 16130
GGTGCAGAGAGCAGCCCCAGAGGCCATGGAAAGAAGTAGCTTGAAACAGGAGGTTCCAGT
-----+-----+-----+-----+-----+

16150 16170 16190
GGCCTCCCAGTCAAGCGAGGGGTGGATCCCTGCCAACACCAGCACCGCAAGGCATGG
-----+-----+-----+-----+-----+

16210 16230 16250
CCCTCTACCTCCCAGTACAGCTCCTTGTCCACTCTCCTGCTTCTCCCACCAGCTGGCT
-----+-----+-----+-----+-----+

16270 16290 16310
GCCTCACCTTGACTTCGCCCTGTTTCCCTGGCTCAGATTGCAGTCCCTGTACCATGC
-----+-----+-----+-----+-----+

16330 16350 16370
TGCCCCCGGAGGCCTGTCAGCCTCTGTCTCACCAAGTTCGGCCCTTGCCACTCCTC
-----+-----+-----+-----+-----+

16390 16410 16430
TGCACAAATCACCTCTGTCACCCCTTGAAGTTCCAAATGCTGGCCCAGCACATTT
-----+-----+-----+-----+-----+

16450 16470 16490
TCACTCCATACCACTGGTCAGCTGGGTGTGGCTGCCCTGTGCAGGGCCCTGCCTTA
-----+-----+-----+-----+-----+

16510 16530 16550

FIG. 29

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ACCCAGTTCTCTGTGACCTGGGTGGCGGAGTGGGAGTCACATAACTAAGCATGG
-----+-----+-----+-----+-----+-----+

16570 16590 16610
CTGTCCTAGGACTCACCTGCACCAGGGCCCTAGGCAGGCAGGCACCTCTGTGCCATGT
-----+-----+-----+-----+-----+

16630 16650 16670
CTGACATAGCCTGGTCTTGGGAGTGCTCCGGCAAGCCAAGGGAGATGGCATGATTGGG
-----+-----+-----+-----+-----+

16690 16710 16730
CCAGAGATGGGGCAGAGGGCATAAACAGACAGGGCAGGGCACCCACTGGCCCCGGGTG
-----+-----+-----+-----+-----+

16750 16770 16790
GCAGCTAACAGGGACCCCTGACAAAGCGAGTTGTGATTGAGGGTCTGTGGCAGAGGAGCAA
-----+-----+-----+-----+-----+

16810 16830 16850
GGTGGCCAGAGCCTGGCGTGTCAAGCACGGAGGGCGCTGCAGAGGGTGGCGGCTGCTTC
-----+-----+-----+-----+-----+

16870 16890 16910
TCATCCCCAGGCGGGAGTCTCAGGGCAGGGGAGAATGTTGAAGGAACATCACAGGAAA
-----+-----+-----+-----+-----+

16930 16950 16970
TGACAAGGCCTGGGGATGGGATGGGACAGTCAAAGATGGCTTGAATCATCAAGGGC
-----+-----+-----+-----+-----+

16990 17010 17030
AGCAGGGCACCCAGGGCAAGGAGAGCAGACATAGCTGCCGAAGGGCGGACATCCAAGG
-----+-----+-----+-----+-----+

17050 17070 17090
TTCTTTGGAAGCTGAGCGATGCCAGCATCTGGAGAGTGCAGGCTGCTGGGGGTGTCAG
-----+-----+-----+-----+-----+

FIG. 29

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17110 17130 17150
AGCCTGGAGGAAATGTTAGGACTAGAGAGAGGTGCCAGCCGAGGGCATGAGGCTCAC
-----+-----+-----+-----+-----+

17170 17190 17210
TTGGAGCCTGGATCCCAAGGCTCCCTGAAGAGGGAGCAGGAAGGGAGCTGAGAGGGTGA
-----+-----+-----+-----+-----+

17230 17250 17270
CTTGGAGCAGATGGGTGCCCAAGAAA~~CT~~CAGTAAACGCAGAA~~CT~~CCCTGGGCTGGACAC
-----+-----+-----+-----+-----+

17290 17310 17330
CATGCTGCGGGGAGGCAATAACCCACTCAGGATCACTGTGCCAACCTCCTGGACTCTTAT
-----+-----+-----+-----+-----+

17350 17370 17390
CACGTTGCTCAGCCCCAAAGATGGCCCACACAGGGACCACCCCTGGCGGCGTTCACCC
-----+-----+-----+-----+-----+

17410 17430 17450
CATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGTGAGTGAGGCACCAG
-----+-----+-----+-----+-----+

17470 17490 17510
GGGGAGGTGGAGAGGGAAAGGGAGAAGGGAAAGGGCTCATGCCTCCTGCTCTCCAGATG
-----+-----+-----+-----+-----+

17530 17550 17570
GGCAGCACCCAGTCACCTTGAGTCCCTATGCCCTCCCCAGCCCCAGGGTCTCCTGCTG
-----+-----+-----+-----+-----+

17590 17610 17630
ACCATATTACAACATTTACCCCTCCACCATTCTCCAGACCCCTGAGAA~~CT~~CATGAGC
-----+-----+-----+-----+-----+

17650 17670 17690

FIG. 29

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CCAGCAGCCACCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGGTAGGCAGG

17710 17730 17750

GACCTGGATTCAAAGCCTCCCCCTCTCATCGCCCACCCCTCCACCTCTCCCACCCCTCAG

17770 17790 17810

TTTGCTCCCCCTAACAGGTTCTGGGCTCAGGTATTATGAAATGAGTTATGACCT
-----+-----+-----+-----+-----+-----+-----+

17830 17850 17870

CTTGGTTATCATGGAGACCAGGATGCTGGAAGCCCCCTGGGCTGGGAGGGAGAAGCTGTG
-----+-----+-----+-----+-----+-----+-----+

17890 17910 17930

GCTTTCTGGATCACTGGTCTCACTGAGTGAGGAGGGGCTCTCGCCACACAGCTTGC

17950 17970 17990

AGCCTGGGGCCCGTCCTTAGGGACAACATATCCTCCTCATTCAGCAGATCAAGTC

18010 18030 18050

CAGATGCCAAGATCCCTGGTAGCTAAATGAACAGATTAAAGAC

18070 18090 18110

AGGTGGCCACTGACAGCCACTCCAGGAAC TTGA ACTGCAGGGCAGAGCCAGTGAATCAC
-----+-----+-----+-----+-----+-----+-----+

18130 18150 18170

CGGACCTCCAGCACCTGCAGGCAGCTTGGAAAGTTCTTCCCCGAGTGGAGCTTCGACCCA
-----+-----+-----+-----+-----+-----+-----+-----+

18190 18210 18230

CCCACTCCAGGAACCCAGAGGCCACATTAGAAGTTCCTGAGGGCTGGAGAACACTGCTGGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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18250 18270 18290
CACACTCTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCCCTGACC
-----+-----+-----+-----+-----+

18310 18330 18350
TCCCTCACCAAGTGGAGGCTGGGTAGTGCTGGCCATCCAAAAGGGCTCTGTCCCTGGGAGT
-----+-----+-----+-----+-----+

18370 18390 18410
CTGGTGTGTCTCCTACATGCAATTCCACGGACCCAGCTCTGTGGAGGGCATGACTGCTG
-----+-----+-----+-----+-----+

18430 18450 18470
GCCAGAAGCTAGTGGCCTGGGCCTATGGTCGACTGAGTCCACACTCCCCTGCAGCC
-----+-----+-----+-----+-----+

18490 18510 18530
TGGCTGGCCTCTGCAAAAAACATAATTGGGGACCTTCCTGTTCTCCCACCC
-----+-----+-----+-----+-----+

18550 18570 18590
TGTCTTCTCCCCTAGGTGGTTCTGAGCCCCACCCCAATCCCAGTGCTACACCTGAGG
-----+-----+-----+-----+-----+

18610 18630 18650
TTCTGGAGCTCAGAATCTGACAGCCTCTCCCCATTCTGTGTGTCGGGGGACAGAGG
-----+-----+-----+-----+-----+

18670 18690 18710
GAACCATTAAAGAAAAGATACCAAAGTAGAAGTCAAAAGAAAGACATGTTGGCTATAGGC
-----+-----+-----+-----+-----+

18730 18750 18770
GTGGTGGCTCATGCCTATAATCCAGCACTTGGGAAGCCGGGTAGGAGGATCACCAGA
-----+-----+-----+-----+-----+

18790 18810 18830

FIG. 29

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GGCAGCAGGTCCACACCAGCCTGGCAACACAGCAAGACACCGCATCTACAGAAAAATT
-----+-----+-----+-----+-----+-----+

18850 18870 18890
TTAAAATTAGCTGGCGTGGTGTACCTGCTAGGCCTAGCTGCTCAGGAGGCTGAAG
-----+-----+-----+-----+-----+-----+

18910 18930 18950
CAGGAGGATCACTTGAGCCTGAGTCACACTGCAGTGAGCTATGGTGGCACCACTGCAC
-----+-----+-----+-----+-----+-----+

18970 18990 19010
TCCAGCCTGGGTGACAGAGCAAGAGCCTGCTCTAAAATAAATTAAAGACATATTA
-----+-----+-----+-----+-----+-----+

19030 19050 19070
ACTTGGACCTTGGTTAGCTTTCTGTATGTAATTCAACCCATGGGTGCCCTGAGGAC
-----+-----+-----+-----+-----+-----+

19090 19110 19130
CCACACGGGTGGTGGTGGCGGGGTGGTGGTGGTGGGTGGCTGACGGGTGGTG
-----+-----+-----+-----+-----+-----+

19150 19170 19190
GCTGGCAGGCCAGCCTAGATGGCAGCCAGAGCCCCAGGCATGTGTCTGGCACAGGACG
-----+-----+-----+-----+-----+-----+

19210 19230 19250
GTGTTGCCTAGTTGAACACCCCTTTGCTCTGTCACTCCTGCCCTGGCGTTCAC
-----+-----+-----+-----+-----+-----+

19270 19290 19310
ATTCTCCCATTGCTTCATGCAAGAGCTGCTGAGTGGCTATATCAGCCAGCTGTTGCCGC
-----+-----+-----+-----+-----+-----+

19330 19350 19370
ATAACAAAACCATCCAAAAGTGAAGTGCAGGGAGGCAACTCACCTGGCTCCACTCCA
-----+-----+-----+-----+-----+-----+

FIG. 29

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-----+-----+-----+-----+-----+
19390 19410 19430
CAAGCCCAAGGGGCCAGGTGAGAGTGCTCTCTAAAGCCCCCTGCCTCAGTTGTTAGTT
-----+-----+-----+-----+-----+

19450 19470 19490
GCAAAATTTAATTATGAAGGTGACTGATGACACAGAGGCCAATGCTGTTGAAATAAGT
-----+-----+-----+-----+-----+

19510 19530 19550
TATTACTCACAGTTCCCACCATGCAGGGCACAGTGGGAGGCACAGGTTGGTCCAG
-----+-----+-----+-----+-----+

19570 19590 19610
GGACAGAACATCAGGAGCGAGTGGAAAGGCCACAGGCCACAGTGCCTTCCACTGG
-----+-----+-----+-----+-----+

19630 19650 19670
GGAGGCAAGGCAGGCCAGGGAAAGAGGGTAGGATTGGCATTTGAATCATTCTGGTGGGG
-----+-----+-----+-----+-----+

19690 19710 19730
TTTGGGCGTGGGTTGGCTCTAATTGTCTGGTAGGTGCCTGCCCTGAGCTGGTTA
-----+-----+-----+-----+-----+

19750 19770 19790
GGGCAGGGAAATACTGGTTCGTATGTGAGAGTCCTGAAGGGGTGGTTGGTGTATG
-----+-----+-----+-----+-----+

19810 19830 19850
GACTCAAGACTGGTCGGTTGCATATGAAAGGCATGAGTTCTGATCTCCAGGAATC
-----+-----+-----+-----+-----+

19870 19890 19910
AAGCAGTTCTCTCCAGCCAACAAGCCCCACCCCGAGATGTTAACCATCATAAAATAG
-----+-----+-----+-----+-----+

FIG. 29

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19930 19950 19970
AGAATCTAAGGCCAGGCATGGTGGCTACGCCTGTAATCCAGCACTTGGGAGGCCAAG
-----+-----+-----+-----+-----+

19990 20010 20030
GCGGGAGGATCATTGAGGTCAAGTCAGAAGTTGAGACCAGCCTGGCCAATGTGGTGAAACCCC
-----+-----+-----+-----+-----+

20050 20070 20090
ATCTCTACTAAAAATACAAAAATTAGCCCGGTGTGGTGGCACGTGCCTATAATCCCAGCT
-----+-----+-----+-----+-----+

20110 20130 20150
ACTCGGGAGGCTGCGGCAGGAGAACATTGTTGAACATGGGAGGTGGAGGTTGCAGTGAGCT
-----+-----+-----+-----+-----+

20170 20190 20210
GAGATCGTGCCACTGCACTCCAGCCTGGCAACAAGAGCAAGACTCCGTCTCAAAAAAAA
-----+-----+-----+-----+-----+

20230 20250 20270
AAAAAAAAAAAGAGAGACTCTAAAAATACACGTTAATATACCTCCCCGCTCTTACCCCT
-----+-----+-----+-----+-----+

20290 20310 20330
TCAGGAGGGGTGTCTAGACCCCGCGGGACTCCAGCTACAAGGGACCTGGGAGGCCA
-----+-----+-----+-----+-----+

20350 20370 20390
CTCTGCCCTTGGCTAATCCCCAAGACTGCCAGCACCCCTCCACCCCTCTCCATT
-----+-----+-----+-----+-----+

20410 20430 20450
AGTGGCGAACCTGGGAGGCCACGTGGGAAGGAAAGAGGGCTCTAACAGAGGGAGGCC
-----+-----+-----+-----+-----+

20470 20490 20510
AGACTGGGGAGAGGCCCTGTCTGGAGGCCAGGATCACCTGGCTGTGCTGCAGAACTGGAG

FIG. 29

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-----+-----+-----+-----+-----+
20530 20550 20570
AAGAGAAGCTAGCAGAAAGGAGCTGGCATGGGCCAACAGCAGAAAAGCAGGAGGCACG
-----+-----+-----+-----+-----+
20590 20610 20630
CAGAAGTGAUTGGGAAGCAGGAGGGTAGGCATGGACCCTGAGGCTGAGCAGGAGGTACTG
-----+-----+-----+-----+-----+
20650 20670 20690
AGGGGCAGAGTGGACGCTGAGCTGGGGTAGCGAGCGAGGCCAGCTCAGCTGTGACGCC
-----+-----+-----+-----+-----+
20710 20730 20750
TCTGTTGGCCACCCAACCTACCACTGGCTGCCCCGGGAGGAACGGGCTTCCTC
-----+-----+-----+-----+-----+
20770 20790 20810
TGACATTCTGTGGCTGCGGCCATCTGTACACACCTCTCTCTCTGCCCTCCCTGA
-----+-----+-----+-----+-----+
20830 20850 20870
CTTGTGGCACCCACAGACAGGTGGAGAGTGTACCTGCCCTGTGTGGTCAGAGCTGGTT
-----+-----+-----+-----+-----+
20890 20910 20930
TTGAGTTCCCTCCCTACCCCTCTTCCCTCCCACACGCCAAACACAAGAGGATGTGTC
-----+-----+-----+-----+-----+
20950 20970 20990
AGAGGCCTGTGAACCACTCCATCCTGAATAGGGCTGAGCAAATAAGGCTGAG
-----+-----+-----+-----+-----+
21010 21030 21050
ACCTACTGGCTGCGTTCCAGACAGTTACAGCATTGCGTCACAGGATGAGATAGGAG
-----+-----+-----+-----+-----+

FIG. 29

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21070 21090 21110
ATACAGGTCATAAAGACOTTGCTGATAAAATAGTTGCAGTAGGCCAGGCGCGTAGCTC
-----+-----+-----+-----+-----+-----+

21130 21150 21170
ACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGCGGATCACCTGAGGTAGAAGT
-----+-----+-----+-----+-----+

21190 21210 21230
TCGAGACCAGCCTGGCCAACAAGGTGAAACCTCATCTACTAAAAATACAAAAACTAGC
-----+-----+-----+-----+-----+

21250 21270 21290
CAGGCATGGTGGTGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACATCG
-----+-----+-----+-----+-----+

21310 21330 21350
CTTGAAACCCAGGAGGTGGAGGTTGCAGTGAGCTGAGATCATGTCACTGCACTCCAGCCTG
-----+-----+-----+-----+-----+

21370 21390 21410
GAGCGAGACTCCGTCTCAAAACCAAACCAACCAAAAAATCAGCTTGAATATAGAAGC
-----+-----+-----+-----+

21430 21450 21470
TGGCTAAACCCACCAAACCAAGATGGTATGAGAGTGACCTCTGGTCGGTCCCCACTG
-----+-----+-----+-----+-----+

21490 21510 21530
CTACACTCCCACCAAGCACCATGACAGGTTACAGATGCCATGGCAGTATCAGGAAGTTACC
-----+-----+-----+-----+

21550 21570 21590
ATATATGGTCTAAAAGGGGAGACATGAACAAATCCACCCCTGTTAGCAGATCATCCAGA
-----+-----+-----+-----+

21610 21630 21650
AACAAACCATAAAATGGCAACCAGCAGCCCTCAGGGCTGCGCTCTATGGAGTAGCCA

FIG. 29

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-----+-----+-----+-----+-----+

21670 21690 21710

TTCTTTATTCTTTACTTTCTTAATAAAATGTGCTTCACTTATGGACTCGTCTCAAAT
-----+-----+-----+-----+-----+

21730 21750 21770

TCTTCTTGACAGAGATCCAAGAACCCCTCCTGGGTCTGAATCTGGACCCCTTCCGG
-----+-----+-----+-----+-----+

21790 21810 21830

TAACAGATGTCGTAGAGTGAAGCACAACCACTGCAGGGCATTTGTTACATTTGCT
-----+-----+-----+-----+-----+

21850 21870 21890

TCAGCGGCCATGGTTAGCACAGCGAAAGCACATCACAGTCTTGATTCAATTAAAAAA
-----+-----+-----+-----+-----+

21910 21930 21950

TTAGGAAATGGACCACCAAAACACAGACAGATGTACTGAGACAGGATAGGTAGTCAAG
-----+-----+-----+-----+-----+

21970 21990 22010

AAAGTGACCATGTTCTAGGCGCGCAGCAGCAACTGTGGTGACCGTACAGTCAACAAGCCT
-----+-----+-----+-----+-----+

22030 22050 22070

CAGCACTGGCATTGCAATTGAGCTCATTCAGCAAAGCTATCTTCAGCAGGGACTCTCC
-----+-----+-----+-----+-----+

22090 22110 22130

CTCTAGGCAGCAAGCGATTTTATTTACCTGTCTCAAACGTACAGTCTTGTCTTAT
-----+-----+-----+-----+-----+

22150 22170 22190

AACAGTAAGGAACACACCCCTGTGTGGAGATTAAAGATGCTAATGAGGCCAAGCGCAGTT
-----+-----+-----+-----+-----+

FIG. 29

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22210 22230 22250
GCTCACGTCTGTAATTCCAGCAGCTTGGGAGGCAGAGGTGGCGGGTCACTTGAGGTTAG
-----+-----+-----+-----+-----+

22270 22290 22310
AAGTCGAGACCAGCCTGGCAACATGGTGAACCTTGCTCTACTAAAAATACAAAAAT
-----+-----+-----+-----+

22330 22350 22370
TAGCCGGGATGGTGGCGGGCGTCTGTAATCCAGCTACCTGGGAGGCTGAGGCAGAAGA
-----+-----+-----+-----+

22390 22410 22430
ATCGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAG
-----+-----+-----+-----+

22450 22470 22490
CCTGAGGGAGAGAGAGAGCAAGACATCGTTTTGTTGTTGTTGTTGTTGTTGTTGTT
-----+-----+-----+-----+

22510 22530 22550
TTTTAAAAAAAGTCAAAGACAAATCATAGTGGGGCTTCTGGTCACTTTAAATCTT
-----+-----+-----+-----+

22570 22590 22610
AGTGTGAGACTTATTGAGACAGGGCCTACTCTGTTGCCAGGTTGGATGAGATT
-----+-----+-----+-----+

22630 22650 22670
TAACCTCAATTTACTTATAGAATAACTTTGGTTAGTCAAAACAATGCTGTCTCA
-----+-----+-----+-----+

22690 22710 22730
TTCTGATCAGAATAAAACATCAGACAACTCAAGAGAACATTCTGCCAAAATAACTGGCCA
-----+-----+-----+-----+

22750 22770 22790
GGATTCTTCAAAAGTGTCAAGGGTAAAGATAAGGAAAGATGAAGGAACCTCCAGATTGAG

FIG. 29

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-----+-----+-----+-----+-----+-----+

22810 22830 22850
GAGAATAAGGAGACAACTGTGATGTGGGATCCTAGAACATGGATCTTGAACAGAAAAAGGA
-----+-----+-----+-----+-----+-----+

22870 22890 22910
CATTAGTGGAAAATGAGAAATGCAAAACAGTCTACAGTTCTGTTAACAGGATTGTACCA
-----+-----+-----+-----+-----+-----+

22930 22950 22970
AGGTTAGTTCTAGCTGTAATGATTGGACTATGATTAAGTAAGATGGACCATCAGGGGA
-----+-----+-----+-----+-----+-----+

22990 23010 23030
AGCTGGGTGAAGGGTGTAAAGGAAAATGCTTACATTTCCAACCTTCTGCAAGTCTAAAA
-----+-----+-----+-----+-----+-----+

23050 23070 23090
TTAGTCACAATAAGAAGTTAAAATAGGCCAGGCATGGTGGCTCACACCTGTCATCCTA
-----+-----+-----+-----+-----+-----+

23110 23130 23150
GCACTTTGAGAGGCCGAGGTGGGAGGATGGTTGAGCCCAGGAGTTCAAGACCAGCCTGC
-----+-----+-----+-----+-----+-----+

23170 23190 23210
GCAAATAGAGCGAGACCCAACTCTATTCAAAAAAATTTTTAAGTTAAAATAGAATTA
-----+-----+-----+-----+-----+-----+

23230 23250 23270
TATAAAAAGGAAAAGAAAATGCTGTTCATAGCGTTCTAGTTAGCATGGAGAGAC
-----+-----+-----+-----+-----+-----+

23290 23310 23330
CAGGTCTCCCTGGGTGGTTCTGTGTGTTGCTGGGTGTGCCTGGCAGGGCTAGTGTGTT
-----+-----+-----+-----+-----+-----+-----+

FIG. 29

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23350

23370

23390

GGGTCCGTCTAGGCACATTCAAGCGCCGAATCCGTGGTCCCAGGTTACCTGACGGT
-----+-----+-----+-----+-----+

23410

23430

23450

GCAGCCTGGGGTGGAGACTTAATGAGGGGGAGTTGCTGCAGCAAAGGCTCCTCCAG
-----+-----+-----+-----+-----+

23470

23490

23510

GGGTATCAGCGCAGACAGCTGGTTTCACTGTGCTCCTGCTCCAGAGGCCTAGGAAGG
-----+-----+-----+-----+-----+

23530

23550

23570

GGCGCCTATCAGACTAGGACTCTGCCAGCCATCCTCTGTGAAGGTCCAGC
-----+-----+-----+-----+

FIG. 29

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10	30	50
CAGCTATGGGCTGGAGGCCCGAGAGCTCGGGGGACCCGTTGCTGCTGCTACTAC -----+-----+-----+-----+-----+ MetGlyTrpArgProArgArgAlaArgGlyThrProLeuLeuLeuLeuLeuL		
70 90 110		
TGCTGCTGCTCTGCCAGTGCCAGGCCGGGTGCTCAAGGACATATCCCTGGGCAGC -----+-----+-----+-----+-----+ euLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyHisIleProGlyGlnP		
130 150 170		
CAGTCACCCCGCACTGGGTCTGGATGGACAACCCCTGGCGACCGTCAGCCTGGAGGAGC -----+-----+-----+-----+-----+ roValThrProHisTrpValLeuAspGlyGlnProTrpArgThrValSerLeuGluGluP		
190 210 230		
CGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGC -----+-----+-----+-----+-----+ roValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluGlyGlnGluLeuL		
250 270 290		
TTGAGCTGGAGAAGAACCACAGGCTGCTGGCCCCAGGATA <u>CATAGAAACCCACTACGGCC</u> -----+-----+-----+-----+-----+ euGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIleGluThrHis <u>TyrGlyP</u>		
310 330 350		
CAGATGGCAGCCAGTGGTCTGGCCCCAACCACACGGATCATTGCCACTACCAAGGGC -----+-----+-----+-----+-----+ roAspGlyGlnProValValLeuAlaProAsnHisThrAspHisCysHisTyrGlnGlyA		
370 390 410		
GAGTAAGGGCTTCCCCGACTCCTGGTAGTCCTCTGCACCTGCTCTGGATGAGTGGCC -----+-----+-----+-----+-----+ rgValArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyL		
430 450 470		
TGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCCTCCCTGGCCACCCGGGCTCCA -----+-----+-----+-----+-----+ euIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerL		

FIG. 30

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490 510 530
AGGACTTCTAACCCACGAGATCTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCT
-----+-----+-----+-----+-----+
ysAspPheSerThrHisGluIlePheArgMetGluGlnLeuLeuThrTrpLysGlyThrC

550 570 590
GTGGCCACAGGGATCCTGGAACAAAGCGGGCATGACCAGCCTCCTGGTGGTCCCCAGA
-----+-----+-----+-----+-----+
ysGlyHisArgAspProGlyAsnLysAlaGlyMetThrSerLeuProGlyGlyProGlnS

610 630 650
GCAGGGGCAGGCCAGAAGCGCGCAGGACCGGAAGTACCTGGAACTGTACATTGTGGCAG
-----+-----+-----+-----+-----+
erArgGlyArgArgGluAlaArgArgThrArgLysTyrLeuGluLeuTyrIleValAlaA

670 690 710
ACCACACCCTGTTCTGACTCGGACCGAAACTTGAACCACACCAACAGCGTCTCCTGG
-----+-----+-----+-----+-----+
spHisThrLeuPheLeuThrArgHisArgAsnLeuAsnHisThrLysGlnArgLeuLeuG

730 750 770
AAGTCGCCAACTACGTGGACCAGCTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCG
-----+-----+-----+-----+-----+
luValAlaAsnTyrValAspGlnLeuLeuArgThrLeuAspIleGlnValAlaLeuThrG

790 810 830
GCCTGGAGGTGTGGACCGAGCGGGACCGCAGCCCGTCACGCAGGACGCCAACGCCACGC
-----+-----+-----+-----+-----+
lyLeuGluValTrpThrGluArgAspArgSerArgValThrGlnAspAlaAsnAlaThrL

850 870 890
TCTGGGCCTCCTGCAGTGGCGCCGGGGCTGTGGCGCAGCGGCCACGACTCCGCGC
-----+-----+-----+-----+-----+
euTrpAlaPheLeuGlnTrpArgArgGlyLeuTrpAlaGlnArgProHisAspSerAlaG

910 930 950
AGCTGCTCACGGGCCGCGCCTCAGGGGCCACAGTGGCCTGGCGCCCGTCGAGGGCA
-----+-----+-----+-----+-----+
lnLeuLeuThrGlyArgAlaPheGlnGlyAlaThrValGlyLeuAlaProValGluGlyM

FIG. 30

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970 990 1010
 TGTGCCGCGCCGAGAGCTCGGGAGCGTGAGCACGGACCACTCGGAGCTCCCCATCGGCG
 etCysArgAlaGluSerSerGlyGlyValSerThrAspHisSerGluLeuProIleGlyA

 1030 1050 1070
 CCGCAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGCCTCAGGCCACGACCCCCGACG
 laAlaAlaThrMetAlaHisGluIleGlyHisSerLeuGlyLeuSerHisAspProAspG

 1090 1110 1130
 GCTGCTGCGTGGAGGCTGCGGCCGAGTCCGGAGGCTGCCTCATGGCTGCGGCCACCGGGC
 lyCysCysValGluAlaAlaAlaGluSerGlyGlyCysValMetAlaAlaAlaThrGlyH

 1150 1170 1190
 ACCCGTTTCCGCGCGTGTTCAGCGCCTGCAGCCGCCAGCTGCGCGCTTCTTCCGCA
 isProPheProArgValPheSerAlaCysSerArgArgGlnLeuArgAlaPhePheArgL

 1210 1230 1250
 AGGGGGCGCGCTTGCTCTCCAATGCCCGGACCCGGACTCCCGTGCCGCCGGCGC
 ysGlyGlyAlaCysLeuSerAsnAlaProAspProGlyLeuProValProProAlaL

 1270 1290 1310
 TCTGCGGAACGGCTTCTGAAAGCGGGCGAGGAGTGTGACTGCGCCCTGGCCAGGAGT
 euCysGlyAsnGlyPheValGluAlaGlyGluGluCysAspCysGlyProGlyGlnGluC

 1330 1350 1370
 GCCGCGACCTCTGCTGCTTGTCAACAATGCTCGCTGCGCCGGGGCCCAGTGCGCCC
 ysArgAspLeuCysCysPheAlaHisAsnCysSerLeuArgProGlyAlaGlnCysAlaH

 1390 1410 1430
 ACGGGGACTGCTGCGTGCCTGCCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCA
 isGlyAspCysCysValArgCysLeuLeuLysProAlaGlyAlaLeuCysArgGlnAlaM

 1450 1470 1490

FIG. 30

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TGGGTGACTGTGACCTCCCTGAGTTTGACGGGCACCTCCTCCCAGACG
---+-----+-----+-----+-----+-----+
etGlyAspCysAspLeuProGluPheCysThrGlyThrSerSerHisCysProProAspV

1510 1530 1550

TTTACCTACTGGACGGCTCACCTGTGCCAGGGCAGTGGCTACTGCTGGATGGCGCAT
---+-----+-----+-----+-----+
alTyrLeuLeuAspGlySerProCysAlaArgGlySerGlyTyrCysTrpAspGlyAlaC

1570 1590 1610

GTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGCCTGGCTCCCACCCAGCTCCCG
---+-----+-----+-----+-----+
ysProThrLeuGluGlnGlnCysGlnGlnLeuTrpGlyProGlySerHisProAlaProG

1630 1650 1670

AGGCCTGTTCCAGGTGGTGAACCTCTGCAGGAGATGCTCATGGAAACTGCAGGCCAGGACA
---+-----+-----+-----+-----+
luAlaCysPheGlnValValAsnSerAlaGlyAspAlaHisGlyAsnCysGlyGlnAspS

1690 1710 1730

GCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGATGCCCTGTGGAAAGCTGCAGTGCC
---+-----+-----+-----+-----+
erGluGlyHisPheLeuProCysAlaGlyArgAspAlaLeuCysGlyLysLeuGlnCysG

1750 1770 1790

AGGGTGGAAAGCCCAGCCTGCTCGCACCGCACATGGTGCCAGTGGACTCTACCGTTCAACC
---+-----+-----+-----+-----+
lnGlyGlyLysProSerLeuLeuAlaProHisMetValProValAspSerThrValHisL

1810 1830 1850

TAGATGGCCAGGAAGTGACTTGTGGGGAGCCTGGCACTCCCCAGTGGCCAGCTGGACC
---+-----+-----+-----+-----+
euAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLeuAspL

1870 1890 1910

TGCTTGGCCTGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCCAGA
---+-----+-----+-----+-----+
euLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCysGlnS

1930 1950 1970

FIG. 30

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GCAGGCCTGCAGGAAGAATGCCTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACA
 -----+-----+-----+-----+-----+
 erArgArgCysArgAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCysHisS

1990	2010	2030
GCCACGGGTTTCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGCTCCACCC -----+-----+-----+-----+-----+ erHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaProProP		
2050	2070	2090
TCTGTGACAAGCCAGGCTTGCTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGAAAACC -----+-----+-----+-----+-----+ heCysAspLysProGlyPheGlySerMetAspSerGlyProValGlnAlaGluAsnH		
2110	2130	2150
ATGACACCTCCTGCTGCCATGCTCCTCAGCG <u>T</u> CCTGCTGCCTCTGCTCCCAGGGGCCG -----+-----+-----+-----+-----+ isAspThrPheLeuLeuAlaMetLeuLeu <u>SerVal</u> LeuLeuProLeuLeuProGlyAlaG		
2170	2190	2210
GCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCC <u>A</u> TCTGCAGCGATGCAGCTGGGGCT -----+-----+-----+-----+-----+ lyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyC		
2230	2250	2270
GCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACCACCCCTGG -----+-----+-----+-----+-----+ ysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuG		
2290	2310	2330
GCGGCCTCACCC <u>C</u> ATGGAGTTGGCCCCACAGCCACTGGACAG <u>C</u> CTGGCCCCCTGGACC -----+-----+-----+-----+-----+ lyGlyValHisPro <u>Met</u> GluLeuGlyProThrAlaThrGlyGln <u>Pro</u> TrpProLeuAspP		
2350	2370	2390
CTGAGAACTCTCATGAGCCCAGCAGCCACCC <u>T</u> GAGAACGCTCTGCCAGCAGTCTGCCTG -----+-----+-----+-----+-----+ roGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProA		
2410	2430	2450
ACCCCCAAGAT <u>CAAGTCCAGATGCCAAGATCCTGCCTCTGGTAGAGAGTAGCTCCTAAAA</u>		

FIG. 30

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-----+-----+-----+-----+-----+
spProGlnAspGlnValGlnMetProArgSerCysLeuTrpEnd

2470 2490 2510
TGAACAGATTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTGCAGGGG
-----+-----+-----+-----+-----+

2530 2550 2570
CAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAAGTTCTTCCCCG
-----+-----+-----+-----+-----+

2590 2610 2630
AGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCCCTGAGGGC
-----+-----+-----+-----+-----+

2650 2670 2690
TGGAGAACACTGCTGGGCACACTCTCCAGCTCAATAAACCATCAGTCCCAGAACGAAAGG
-----+-----+-----+-----+-----+

2710 2730 2750
TCACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGGTAGTGCTGCCATCCAAAAG
-----+-----+-----+-----+-----+

2770 2790 2810
GGCTCTGTCTGGGAGTCTGGTGTCTCCTACATGCAATTCCACGGACCCAGCTCTGT
-----+-----+-----+-----+-----+

2830 2850 2870
GGAGGGCATGACTGCTGGCCAGAACGCTAGTGGTCCCTGGGGCCCTATGGTTCGACTGAGTC
-----+-----+-----+-----+-----+

2890 2910 2930
CACACTCCCCTGCAGCCTGGCTGGCCTCTGCAAAAAACATAATTGGGGACCTTCCTT
-----+-----+-----+-----+-----+

2950 2970 2990
CCTGTTTCTTCCCACCCCTGTCTCCCTAGGTGGTCCTGAGCCCCACCCCCAATCC
-----+-----+-----+-----+-----+

FIG. 30

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3010 3030 3050
CAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGACAGCCTCTCCCCCATTCTGTGTG
-----+-----+-----+-----+-----+-----+

3070 3090 3110
TGTGGGGGACAGAGGGAACCATTAAGAAAAGATAACCAAAAGTAGAAGTCAAAAGAAAG
-----+-----+-----+-----+-----+-----+

3130 3150 3170
ACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCAGCTTGGGAAGCCGGG
-----+-----+-----+-----+-----+-----+

3190 3210 3230
GTAGGAGGATCACCAAGAGGCCAGCAGGTCCACACCAGCCTGGCAACACAGCAAGACACC
-----+-----+-----+-----+-----+-----+

3250 3270 3290
GCATCTACAGAAAAATTAAAGCTGGCGTGGTGTGTACCTGTAGGCCTAGC
-----+-----+-----+-----+-----+-----+

3310 3330 3350
TGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTGAGTTAACACTGCAGTGAGCTA
-----+-----+-----+-----+-----+-----+

3370 3390 3410
TGGTGGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAAAATAAAT
-----+-----+-----+-----+-----+-----+

3430 3450 3470
TTTAAAAAGACATAA
-----+-----+-----+-----+-----+-----+

3490
AAAAAAA
-----+-----+

FIG. 30

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10 30 50
CGGGCACGGGTCGGCCCAATCCAGCCTGGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG

70 90 110
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGACCCGTTGC
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

130 150 170
TGCTGCTGCTACTACTGCTGCTCTGGCCAGTGCCAGGCCGGGTGCTTCAAGGAC
euLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

190 210 230
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCG
isIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThrV

250 270 290
TCAGCCTGGAGGAGCCGGTCTCGAAGCCAGACATGGGGCTGGTGGCCCTGGAGGCTGAAG
alSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGluG

310 330
GCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACACAGGC
lyGlnGluLeuLeuLeuGluLeuLysAsnHisArg

FIG. 31

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10 30 50
CGGGCACGGGTGGCCGCAATCCAGCCTGGCGGAGCCGGAGTTGCGAGCCGCTGCCTAG

70 90 110
AGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCGGAGAGCTGGGGGACCCGTTGC
MetGlyTrpArgProArgArgAlaArgGlyThrProLeuL

130 150 170
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCCGGGTGCTCAAGGAC
euLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGlyH

190 210
ATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGAC
isIleProGlyGlnProValThrProHisTrpValLeuAspGly

FIG. 32

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10 30 50
GCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCC
MetGlyTrpArgProArgArgAlaArgGlyThrP

70 90 110
CGTGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCAGGCCGGGGTGCCTC
roLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuG

130 150 170
AAGGACATATCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGC
lnGlyHisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpA

190 210 230
GCACCGTCAGCCTGGAGGAGGCCGGTCTCGAACGCCAGACATGGGGCTGGTGGCCCTGGAGG
rgThrValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluA

250 270 290
CTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAAGAACACAGGCTGCTGGCCCCCAGGAT
laGluGlyGlnGluLeuLeuLeuGluLeuLysAsnHisArgLeuLeuAlaProGlyT

310 330 350
ACATAGAAACCACTACGGCCCAGATGGGCAGCCAGTGGTCTGGCCCCAACCACACGG
yrIleGluThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrV

370 390 410
TGAGATGCTTCATGGGCTCTGGGATGCACCGCCAGAGGATCATTGCCACTACCAAGGGC
alArgCysPheHisGlyLeuTrpAspAlaProProGluAspHisCysHisTyrGlnGlyA

430 450 470
GAGTAAGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTGGCC
rgValArgGlyPheProAspSerTrpValValLeuCysThrCysSerGlyMetSerGlyL

490 510 530
TGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGCCACCCGGGGCTCCA
euIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrpProProArgGlySerL

550
AGGACTTCTCAACCCACGAGAT
ysAspPheSerThrHisGlu

FIG. 33

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10

30

50

GAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTGGGGACCCGTTG
MetGlyTrpArgProArgArgAlaArgGlyThrProLeu

70

90

110

CTGCTGCTGCTACTACTGCTGCTCTGCCAGTGCCAGGCGCCGGGTGCTCAAGGA
LeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGly

130

150

170

CATATCCCTGGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACC
HisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThr

190

210

230

GTCAGCCTGGAGGAGCCGGTCTGAAGGCCAGACATGGGCTGGTGGCCCTGGAGGCTGAA
ValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGlu

250

270

290

GGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCATGGCTGATCACCTCAGCAGGAAT
GlyGlnGluLeuLeuLeuGluLeuGluLysAsnHisGlyLeuIleThrLeuSerArgAsn

310

330

350

GCCAGCTATTATCTGCGTCCCTGGCCACCCGGGCTCCAAGGACTTCTCAACCCACGAG
AlaSerTyrTyrLeuArgProTrpProProArgGlySerLysAspPheSerThrHisGlu

AT

FIG. 34

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10

30

50

GAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTGGGGGACCCGTTG
MetGlyTrpArgProArgArgAlaArgGlyThrProLeu

70

90

110

CTGCTGCTGCTACTACTGCTGCTCTGGCCAGTGCCAGGCGCCGGGTGCTCAAGGA
LeuLeuLeuLeuLeuLeuLeuLeuTrpProValProGlyAlaGlyValLeuGlnGly

130

150

170

CATATCCCTGGCAGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACC
HisIleProGlyGlnProValThrProHisTrpValLeuAspGlyGlnProTrpArgThr

190

210

230

GTCAGCCTGGAGGAGCCGGTCTGAAGCCAGACATGGGCTGGTGGCCCTGGAGGCTGAA
ValSerLeuGluGluProValSerLysProAspMetGlyLeuValAlaLeuGluAlaGlu

250

270

290

GGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACACAGGCTGCTGGCCCCAGGATAACATA
GlyGlnGluLeuLeuGluLeuGluLysAsnHisArgLeuLeuAlaProGlyTyrIle

310

330

350

GAAACCCACTACGGCCCAGATGGGCAGCCAGTGCTGGCCCCAACACACGGATCAT
GluThrHisTyrGlyProAspGlyGlnProValValLeuAlaProAsnHisThrAspHis

370

390

410

TGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGTAGTCCTCTGCACCTGC
CysHisTyrGlnGlyArgValArgGlyPheProAspSerTrpValValLeuCysThrCys

430

450

470

TCTGGGATGAGTGGCCTGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGG
SerGlyMetSerGlyLeuIleThrLeuSerArgAsnAlaSerTyrTyrLeuArgProTrp

490

510

CCACCCCGGGCTCCAAGGACTTCTCAACCCACGAGAT
ProProArgGlySerLysAspPheSerThrHisGlu

FIG. 35

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10 30 50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110
GGGCCTGGCTCCCACCCAGCTCCGAGGCCTGTTCCAGGTGGTAACTCTGCCGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

130 150 170
TGCTCATGGAAACTGCGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGGA
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

190 210 230
TGCCCTGTGGAAAGCTGCAGTGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCGCACAT
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

250 270 290
GGTGCCAGTGGACTCTACCGTTCACCTAGATGCCAGGAAGTGACTTGTCCGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

310 330 350
GGCACTCCCCAGTGCCAGCTGGACCTGCTGGCCTGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuValGluProGlyThrGl

370 390 410
GTGTGGACCTAGAATGGTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGC
nCysGlyProArgMetValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAl

430 450 470
TCCACCCCTCTGTGACAAGCCAGGCTTGGCAGCATGGACAGTGGCCCTGTGCAGGC
aProProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAl

490
TGAAAACCATGACACCTTCCTGC
aGluAsnHisAspThrPheLeu

FIG. 37

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10 30 50
CAGTGGCTACTGCTGGGATGGCGCATGTCACGCTGGAGCAGCAGTGCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110
GGGCCCTGGCTCCCACCCAGCTCCCGAGGCCTGTTCCAGGTGGTGAACTCTGGGGAGA
pGlyProGlySerHisProAlaProGluAlaCysPheGlnValValAsnSerAlaGlyAs

130 150 170
TGCTCATGGAAACTGCGGCCAGGACAGCGAGGGCCACTTCCTGCCCTGTGCAGGGAGGG
pAlaHisGlyAsnCysGlyGlnAspSerGluGlyHisPheLeuProCysAlaGlyArgAs

190 210 230
TGCCCTGTGTGGGAAGCTGCAGTGCAGGCCAGGGTGGAAAGCCCAGCCTGCTCGCACCG
pAlaLeuCysGlyLysLeuGlnCysGlnGlyGlyLysProSerLeuLeuAlaProHisMe

250 270 290
GGTGCCAGTGGACTCTACCGTTCACCTAGATGCCAGGAAGTGACTTGTGGGGAGCCTT
tValProValAspSerThrValHisLeuAspGlyGlnGluValThrCysArgGlyAlaLe

310 330 350
GGCACTCCCCAGTGCCAGCTGGACCTGCTTGGCCTGGCCTGGTAGAGCCAGGCACCCA
uAlaLeuProSerAlaGlnLeuAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGl

370 390 410
GTGTGGACCTAGAATGGTGTGCCAGAGCAGGGCGCTGCAGGAAGAATGCCCTCCAGGAGCT
nCysGlyProArgMetValCysGlnSerArgArgCysArgLysAsnAlaPheGlnGluLe

430 450 470
TCAGCGCTGCCCTGACTGCCACAGCCACGGGGTTGCAATAGCAACCATAACTGCCA
uGlnArgCysLeuThrAlaCysHisSerHisGlyValCysAsnSerAsnHisAsnCysHi

490 510 530
CTGTGCTCCAGGCTGGCTCCACCCCTCTGTGACAAGCCAGGCCTTGGTGGCAGCAGGAA
sCysAlaProGlyTrpAlaProProPheCysAspLysProGlyPheGlySerMetAs

550 570
CAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCCTGC
pSerGlyProValGlnAlaGluAsnHisAspThrPheLeu

FIG. 38

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10 30 50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110
GGGCCCTGATGCCAGGAAGTGACTGTGGGGAGCCTGGCACTCCCCAGTGCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

130 150 170
GGACCTGCTTGGCCTGGCCTGGTAGAGGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

190 210 230
CCAGAGCAGGCCCTGCAGGAAGAACGCTTCAGGAGCTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

250 270 290
CCACAGCCACGGGGTTTGAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

310 330 350
ACCCCTCTGTGACAAGCCAGGCTTGGTGGCAGCATTGGACAGTGGCCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

370
AAACCATGACACCTTCCTGC
uAsnHisAspThrPheLeu

FIG. 39

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10 30 50
GGCCTGGTGTGCTACCGACTCCCAGGAGCCATCTGCAGCGATGCAGCTGGGCTGCAG
AlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTrpGlyCysAr

70 90 110
AAGGGACCCTGCGTGCAGTGGCCCCAAAGATGGCCCACACAGGGACCACCCCTGGCGG
gArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisProLeuGlyGl

130 150 170
CGTTCACCCCATGGAGTTGGGCCAACAGCCACTGGACAGCCCTGGCCCTGGACCCCTGA
yValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLeuAspProGl

190 210 230
GAACCTCATGAGCCCAGCAGCCACCCCTGAGAAGCCTCTGCCAGCAGTCGCCTGACCC
uAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSerProAspPr

250 270 290
CCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCTAAAAT
oGlnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd

310
GAACAGATTAAAGACAGGTGGCC

FIG. 40

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10	30	50
CAGTGGCTACTGCTGGGATGGCCATGTCCCACGCTGGACCAGCAGTGCCAGCAGCTCTG SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr		
70	90	110
GGGGCCTGATGGCCAGGAAGTGACTTGTGGGGAGCCTTGGCACTCCCCAGTGCCAGCT pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe		
130	150	170
GGACCTGCTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG uAspLeuLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy		
190	210	230
CCAGAGCAGGCCCTGCAGGAAGAACGCTTCAGGAGCTTCAGCGCTGCCACTGCC sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy		
250	270	290
CCACAGGCCACGGGGTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCC sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr		
310	330	350
ACCCTCTGTGACAAGCCAGGCTTGGTGGCAGCATGGACAGTGGCCCTGTGCAGGCTGA oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaG		
370	390	410
AAACCATGACACCTTCCTGCTGGCCATGCTCCTCAGCGTCCTGCTGCCTCTGCTCCCAGG uAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGl		
430	450	470
GGCCGGCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCCACAGCGATGCGAGCTG yAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTr		
490	510	530
GGGCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGATGGCCCACACAGGGACCACCC pGlyCysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisPr		
550	570	590
CCTGGCGGGCGTTCACCCCATGGAGTTGGCCCCACAGCCACTGGACAGCCCTGGCCC oLeuGlyGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLe		
610	630	650
GGACCTGAGAACTCTCATGAGCCAGCAGCCACCCCTGAGAACGCTCTGCCAGCAGTCTC uAspProGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSe		
670	690	710
GCCTGACCCCAAGCAGATCAAGTCCAGATGCCAGATGCCAGATCCTGCCCTCTGGTGAGAGGTAGC rProAspProGlnAlaAspGlnValGlnMetProArgSerCysLeuTrpEnd		
730	750	
TCCTAAAAATGAACAGATTAAAGACAGGGTGGCC		

FIG. 41

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FIG. 42

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CCATCTGCAGCGATGCAGCTGGGGCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGA
aHisLeuGlnArgCysSerTrpGlyCysArgArgAspProAlaCysSerGlyProLysAs

730

750

770

TGGCCCACACAGGGACCACCCCTGGCGGCCGTTCACCCATGGAGTTGGGCCAACAGC
pGlyProHisArgAspHisProLeuGlyGlyValHisProMetGluLeuGlyProThrAl

790

810

830

CACTGGACAGCCCTGGCCCTGGACCCTGAGAACTCTCATGAGCCCAGCAGCCACCCCTGA
aThrGlyGlnProTrpProLeuAspProGluAsnSerHisGluProSerSerHisProGl

850

870

890

GAAGCCTCTGCCAGCAGTCTGCCCTGACCCCCAAGATCAAGTCCAGATGCCAAGATCCTG
uLysProLeuProAlaValSerProAspProGlnAspGlnValGlnMetProArgSerCy

910

930

950

CCTCTGGTAGAGGGTAGCTCTAAATGAACAGATTAAAGACAGGGTGCCACTGACAGC
sLeuTrpEnd

970

990

1010

CACTCCAGGAACCTGAACCTGCAGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTG

1030

1050

1070

CAGGCAGCTTGGAAAGTTCTCCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCA

1090

1110

1130

GAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTGGCACACTCTCCAGCTCAA

1150

TAAACCATCAGTCC

rt772

FIG. 42

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10 30 50
CAGTGGCTACTGCTGGGATGGCGCATGTCCCACGCTGGAGCAGCAGTGCCAGCAGCTCTG
SerGlyTyrCysTrpAspGlyAlaCysProThrLeuGluGlnGlnCysGlnGlnLeuTr

70 90 110
GGGGCCTGATGCCAGGAAGTGACTTGTGGGGAGCCTGGCACTCCCCAGTGCCCAGCT
pGlyProAspGlyGlnGluValThrCysArgGlyAlaLeuAlaLeuProSerAlaGlnLe

130 150 170
GGACCTGCTGGCCTGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTG
uAspLeuLeuGlyLeuGlyLeuValGluProGlyThrGlnCysGlyProArgMetValCy

190 210 230
CCAGAGCAGGGCGTGCAGGAAGAACGCTTCAGGAGCTTCAGCGCTGCCTGACTGCCTG
sGlnSerArgArgCysArgLysAsnAlaPheGlnGluLeuGlnArgCysLeuThrAlaCy

250 270 290
CCACAGCCACGGGTTGCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGCTCC
sHisSerHisGlyValCysAsnSerAsnHisAsnCysHisCysAlaProGlyTrpAlaPr

310 330 350
ACCCTTCTGTGACAAGCCAGGCTTGGTGGCAGCATGGACAGTGGCCTGTGCAGGCTGA
oProPheCysAspLysProGlyPheGlyGlySerMetAspSerGlyProValGlnAlaGl

370 390 410
AAACCATGACACCTTCCTGCTGGCATGCTCCTCAGCGTCTGCTGCCTCTGCTCCCAGG
uAsnHisAspThrPheLeuLeuAlaMetLeuLeuSerValLeuLeuProLeuLeuProGl

430 450 470
GGCCGGCCTGGCCTGGTGTGCTACCGACTCCCAGGAGCCATCTGCAGCGATGCAGCTG
yAlaGlyLeuAlaTrpCysCysTyrArgLeuProGlyAlaHisLeuGlnArgCysSerTr

490 510 530
GGGCTGCAGAAGGGACCCCTGCGTGCAGTGGCCCCAAAGATGGCCCACACAGGGACCACCC
pGlyCysArgArgAspProAlaCysSerGlyProLysAspGlyProHisArgAspHisPr

550 570 590

FIG. 43

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CCTGGCGGCCGTTCACCCATGGAGTTGGCCCCACAGCCACTGGACAGCCCTGGCCCT
oLeuGlyValHisProMetGluLeuGlyProThrAlaThrGlyGlnProTrpProLe

610 630 650

GGACCCCTGAGAACTCTCATGAGCCCAGCAGCCACCCTGAGAAGCCTCTGCCAGCAGTCTC
uAspProGluAsnSerHisGluProSerSerHisProGluLysProLeuProAlaValSe

670 690 710

GCCTGACCCCCAACAGATCAAGTCCAGATGCCAAGATCCTGCCTCTGGTGAGAGGTAGCTCC
rProAspProGlnAspGlnValGlnMetProArgSerCysLeuTrpEnd

730 750 770

TAAAATGAACAGATTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTG

790 810 830

AGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAAGTTCTT

850 870 890

CCCCGAGTGGAGCTTCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTG

910 930 950

AGGGCTGGAGAACACTGCTGGCACACTCTCCAGCTCAATAAACCATCAGTCC

FIG. 43